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OM protein - protein search, using sw model

Run on: July 12, 2001, 17:12:38 ; Search time 13.8 seconds
(without alignments)
849.578 Million cell updates/sec

Title: US-09-294-539-4

Perfect score: 2952

Sequence: 1 MEPPTSHTVNAFSDSDASV.....RSLGSSSSSTSGAIRPRR 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1276	43.2	593	2	US-08-989-478-2
2	1276	43.2	593	3	US-08-996-685-2
3	1276	43.2	593	3	US-08-880-179-3
4	1270	43.0	593	2	US-08-989-478-8
5	1270	43.0	593	3	US-08-996-685-8
6	1188.5	40.3	521	2	US-08-989-478-12
7	1188.5	40.3	521	3	US-08-996-685-12
8	1134	38.4	469	2	US-08-989-478-10
9	1134	38.4	469	3	US-08-996-685-10
10	1052.5	35.7	397	2	US-08-989-478-14
11	1052.5	35.7	397	3	US-08-996-685-14
12	751	25.4	261	2	US-08-989-478-16
13	751	25.4	261	3	US-08-996-685-16
14	133	4.5	1088	4	US-09-082-059-2
15	127	4.3	1839	2	US-09-172-977-4
16	126	4.3	843	2	US-09-172-977-3
17	124.5	4.2	300	2	US-08-897-340-32
18	124.5	4.2	300	4	US-09-252-329-32
19	122	4.1	41	2	US-08-989-478-17
20	122	4.1	41	2	US-08-989-478-19
21	122	4.1	41	2	US-08-989-478-21
22	122	4.1	41	2	US-08-989-478-23
23	122	4.1	41	3	US-08-996-685-17
24	122	4.1	41	3	US-08-996-685-19
25	122	4.1	41	3	US-08-996-685-21
26	122	4.1	41	3	US-08-996-685-23
27	122	4.1	41	3	US-08-880-179-4

28 122 4.1 41 3 US-08-880-179-6 Sequence 6, Appl1
29 122 4.1 41 3 US-08-880-179-8 Sequence 8, Appl1
30 122 4.1 41 3 US-08-880-179-10 Sequence 10, Appl1
31 119.5 4.0 359 2 US-08-388-756-2 Sequence 2, Appl1
32 119.5 4.0 359 2 US-08-748-428-2 Sequence 2, Appl1
33 119.5 4.0 359 2 US-08-802-322-3 Sequence 3, Appl1
34 119.5 4.0 389 2 US-08-802-322-14 Sequence 14, Appl1
35 116 3.9 787 4 US-09-188-930-334 Sequence 334, Appl1
36 111.5 3.8 356 2 US-08-903-851-2 Sequence 2, Appl1
37 110 3.7 418 2 US-08-978-182-5 Sequence 5, Appl1
38 110 3.7 418 2 US-09-205-681-5 Sequence 5, Appl1
39 110 3.7 1745 2 US-09-031-485-33 Sequence 33, Appl1
40 110 3.7 1745 2 US-08-847-429A-33 Sequence 33, Appl1
41 110 3.7 1745 3 US-09-065-474-33 Sequence 33, Appl1
42 108 3.7 969 1 US-08-365-689-3 Sequence 3, Appl1
43 108 3.7 969 1 US-07-747-781-3 Sequence 3, Appl1
44 108 3.7 969 1 US-08-145-138A-3 Sequence 3, Appl1
45 108 3.7 969 5 PCT-US92-06888-3 Sequence 3, Appl1

ALIGNMENTS

RESULT 1

US-08-989-478-2

; Sequence 2, Application US/08989478

; Patent No. 5986082

; GENERAL INFORMATION:

; APPLICANT: Uknes, Scott

; APPLICANT: Hunt, Michelle

; APPLICANT: Steiner, Henry-York

; APPLICANT: Ryals, John

; TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING

; NUMBER OF INVENTION: DISEASE RESISTANCE IN PLANTS

; NUMBER OF INVENTION: 32

; CORRESPONDENCE ADDRESS:

; ADDRESS: No. 5986082artis Corporation

; STREET: 3054 Cornwallis Road

; CITY: Research Triangle Park

; STATE: No. 5986082th Carolina

; COUNTRY: USA

; ZIP: 27709

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/989,478

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/033,177

; FILING DATE: 13-DEC-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/034,379

; FILING DATE: 27-DEC-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/034,382

; FILING DATE: 27-DEC-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/034,730

; FILING DATE: 10-JAN-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/035,021

; FILING DATE: 10-JAN-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/035,022

; FILING DATE: 10-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Meigs, J. Timothy

; REGISTRATION NUMBER: 38,241

; REFERENCE/DOCKET NUMBER: PF/5-21214/PI/CGC1911

TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-989-478-2

Query Match 43.2%; Score 1276; DB 2; Length 593;
Best Local Similarity 47.2%; Pred. No. 1.le-121;
Matches 273; Conservative 113; Mismatches 165; Indels 28; Gaps 9;

QY 5 TSHVTNAFSDSDASVEGDADADAEALRLSDNLAAAFSPEDFAFLADARIAVPGG 64
DB 17 TSFVATDNTDSSIVYLAEEQVLTGPDVSALQLLSNFSFVDSFDD--FYSDAKLVL--- 71
QY 65 GGGGDLRVHRCVLSARSFPLRGVFAARRAAAAGGGGDSERLELRLGGGEEVEVG 124
DB 72 -SDGREVSFHRVLSARSFPLRGVFAARRAAAAGGGGDSERLELRLGGGEEVEVG 124
QY 125 YEALRLVLDLYSGRVGDLPAKACLCVDEDCAHVGHCHPAVAFMAQVFAAFTFOVAELTN 184
DB 125 FDSVTVLAVYSSRVRRPPKGVSCADENCHVACRAVDQFMLEVLYLAFIKIPELIT 184
QY 185 LQORLLDVLKVEVDNLLILSVANLCKNSCKMLLECLDCLMVRNSLDMITLESPLPD 244
DB 185 LYORHLDDVVKVIEDTLVLKLANICGKACMLDKRCKEIIIVKSNVDMVLSKSLPEE 244
QY 245 VIKQITDRLSLGLSPENKGNPKHVRIRHALSDSDVDELVRMLLTGOTNLLDDAFALH 304
DB 245 LVKEIIDRKEGLGKPVK----KHSNVHRLSDSDVDELVRMLLTGOTNLLDDAFALH 300
QY 305 YAYEHGDSKTTTLLDLALADVNHNRPRGYTVLHIAARREPKIIVSLITKGARPDVTF 364
DB 301 FAYAYCNVKTATDLLKLDLADVNHNRPRGYTVLHIAARREPKIIVSLITKGARPDVTF 360
QY 365 DGRKAVOISRLTKQDYGVEGTEGSPKDLICILILEQAEERROPOLGEASVSLAMAGE 424
DB 361 EGRALMIAQATMAVECNINPEQCKSLKGLCVLEIQEQRKQIPDRVPPSPFAVAAD 420
QY 425 SLRGLLYLNRVALARIMPEMARVAMDAQVDGTLFENLGSANPPPPR---QRTTV 480
DB 421 ELKWLTLNLRVALAQLRLEPTQAQAAAEIEMKGTCEFIIVTS---LEPDRLTGKRTSP 477
QY 481 DLNESPFIKKEHLARMTALSKTVELGKFPFRCNSVLDKIMD--DETDPVSLGRDTSAEK 539
DB 478 GVKIAPFRILEEHQSRKLSKTVELGKFPFRCNSVLDKIMD--DETDPVSLGRDTSAEK 537
QY 540 R-----KRFHLDVLOKAFHDEKREMDRSLSSSSSTS 574
DB 538 RLQKKRYMEIQETLKAFFEDNLELGNLSLTSTSTS 576

US-08-996-685-2

Query Match 43.2%; Score 1276; DB 3; Length 593;
Best Local Similarity 47.2%; Pred. No. 1.le-121;
Matches 273; Conservative 113; Mismatches 165; Indels 28; Gaps 9;

QY 5 TSHVTNAFSDSDASVEGDADADAEALRLSDNLAAAFSPEDFAFLADARIAVPGG 64
DB 17 TSFVATDNTDSSIVYLAEEQVLTGPDVSALQLLSNFSFVDSFDD--FYSDAKLVL--- 71
QY 65 GGGGDLRVHRCVLSARSFPLRGVFAARRAAAAGGGGDSERLELRLGGGEEVEVG 124
DB 72 -SDGREVSFHRVLSARSFPLRGVFAARRAAAAGGGGDSERLELRLGGGEEVEVG 124
QY 125 YEALRLVLDLYSGRVGDLPAKACLCVDEDCAHVGHCHPAVAFMAQVFAAFTFOVAELTN 184

Db 125 FDSVTVLAVYSSRVRRPPKGVSECADENCCVACRPVAFDMFLVLYLAFIKPIELIT 184
QY 185 LFORRLDVLKVEVDNLLILSVANLCKSKMKLLERCLDMVVRNLDMLITKSLPPD 244
Db 185 LYORHLLDVLKVEVDNLLILSVANLCKSKMKLLERCLDMVVRNLDMLITKSLPPD 244
QY 245 VIKQIIDARLSGLISPKENKGFNKHVRIRHRLDSDVVELVRLMTEGOTNLDLDAFALH 304
Db 245 LKKEIIDRRKELGLEVPKVK---KHVSNNVKALDSDDIELVKKLLKEDHTNLDLDAFALH 300
QY 305 YAVEHCOSKITTELLDLALADVNHRRPRGYTVLHIAARRREPKEIIVSLTKGARPADVT 364
Db 301 FAVAYCNVATATDLDLADVNHRRPRGYTVLHIAARRREPKEIIVSLTKGARPADVT 360
QY 365 DGRKAVQISKRLTKQDYGVTGEGPKSPKDRLCIELEQAEERDDPQLGEASVSLAMAGE 424
Db 361 EGRALMIKAKATMAVECNIPQCKHSLKGRCLVCEIQEDKREQIPRDVPPSFAVAAD 420
QY 425 SLRGLLYLENVALARIMPPMEARVAMDIAQVDGTLEFNLGSGANPPPER---QRTTV 480
Db 421 ELKMTLLDLLENVALAQLRFPTEAQAAMEIAEMKGTCEFTVTS---LEPDLTGTRTSP 477
QY 481 DLNESPFIMKEEHLARMTALSKTVELGKRFPPRCNVLDKIMD-DETDPVSLGRDTSAEK 539
Db 478 GVKIAPFRILEEHQSRKALKSKTVELGKRFPPRCNVLDKIMD-DETDPVSLGRDTSAEK 537
QY 540 R---KRFHDLQDLQKAFHEKEDKEENDRSGLSLSSSSSTS 574
Db 538 RLQKKORYMEIQETLKKAFSEDNLELGNSSSLTDSSTS 576

RESULT 3

US-08-880-179-3
; Sequence 3, Application US/08880179
; Patent No. 6091004
; GENERAL INFORMATION:
; APPLICANT: Ryals, John
; APPLICANT: Delaney, Terry
; APPLICANT: Friedrich, Leslie
; APPLICANT: Weymann, Kristiana
; APPLICANT: Lawton, Kay
; APPLICANT: Ellis, Daniel
; APPLICANT: Uknes, Scott
; APPLICANT: Jesse, Taco
; APPLICANT: Vos, Pieter
; TITLE OF INVENTION: GENE ENCODING A PROTEIN INVOLVED IN THE
; TITLE OF INVENTION: SIGNAL TRANSDUCTION CASCADE LEADING TO SYSTEMIC ACQUIRED RESIS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6091004artis Corporation
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,179
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1909
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 593 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-880-179-3

Query Match 43.2%; Score 1276; DB 3; Length 593;
Best Local Similarity 47.2%; Pred. No. 1,1e-121;
Matches 273; Conservative 113; Mismatches 165; Indels 28; Gaps 9;

QY 5 TSHVTNFAFSDSDASVEEGDADADADVEALRRSLDNLAAAFRSPEDFAFLADARIAVPGG 64
Db 17 TSPVATDNTDSSIVYLAEEQVLTGPDVSAQLLLSNFESVFSDPD--FSDAKLVL--- 71
QY 65 GGGGDLRVHRCVLSARSFPLRGVFAARRAAAAGGGGDSERLEURELLGGGEEVEVG 124
Db 72 -SDGREVSFHRVLSARSFPLRGVFAARRAAAAGGGGDSERLEURELLGGGEEVEVG 124
QY 125 YEALRLVLDLYISGRVGDLPKAAACLCVDECAHVGHCHPAVAFMAQVLFASSTFQVAVELTN 184
Db 125 FDSVTVLAVYSSRVRRPPKGVSECADENCCVACRPVAFDMFLVLYLAFIKPIELIT 184
QY 185 LFORRLDVLKVEVDNLLILSVANLCKSKMKLLERCLDMVVRNLDMLITKSLPPD 244
Db 185 LYORHLLDVLKVEVDNLLILSVANLCKSKMKLLERCLDMVVRNLDMLITKSLPPD 244
QY 245 VIKQIIDARLSGLISPKENKGFNKHVRIRHRLDSDVVELVRLMTEGOTNLDLDAFALH 304
Db 245 LKKEIIDRRKELGLEVPKVK---KHVSNNVKALDSDDIELVKKLLKEDHTNLDLDAFALH 300
QY 305 YAVEHCOSKITTELLDLALADVNHRRPRGYTVLHIAARRREPKEIIVSLTKGARPADVT 364
Db 301 FAVAYCNVATATDLDLADVNHRRPRGYTVLHIAARRREPKEIIVSLTKGARPADVT 360
QY 365 DGRKAVQISKRLTKQDYGVTGEGPKSPKDRLCIELEQAEERDDPQLGEASVSLAMAGE 424
Db 361 EGRALMIKAKATMAVECNIPQCKHSLKGRCLVCEIQEDKREQIPRDVPPSFAVAAD 420
QY 425 SLRGLLYLENVALARIMPPMEARVAMDIAQVDGTLEFNLGSGANPPPER---QRTTV 480
Db 421 ELKMTLLDLLENVALAQLRFPTEAQAAMEIAEMKGTCEFTVTS---LEPDLTGTRTSP 477
QY 481 DLNESPFIMKEEHLARMTALSKTVELGKRFPPRCNVLDKIMD-DETDPVSLGRDTSAEK 539
Db 478 GVKIAPFRILEEHQSRKALKSKTVELGKRFPPRCNVLDKIMD-DETDPVSLGRDTSAEK 537
QY 540 R---KRFHDLQDLQKAFHEKEDKEENDRSGLSLSSSSSTS 574
Db 538 RLQKKORYMEIQETLKKAFSEDNLELGNSSSLTDSSTS 576

RESULT 4
US-08-989-478-8
; Sequence 8, Application US/08989478
; Patent No. 5986082
; GENERAL INFORMATION:
; APPLICANT: Uknes, Scott
; APPLICANT: Hunt, Michelle
; APPLICANT: Steiner, Henry-York
; APPLICANT: Ryals, John
; TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
; TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5986082artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 5986082th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:

Thu Jul 12 18:51:25 2001

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/989,478
FILING DATE: 27-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21214/PL/CGC1911
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-989-478-8

Query Match 43.0%; Score 1270; DB 2; Length 593;
Best Local Similarity 47.0%; Pred. No. 4.6e-121;
Matches 272; Conservative 113; Mismatches 166; Indels 28; Gaps 9;

QY 5 TSHVTNAFSDSDSASVEEGDADADAEALRLRLSDNLAAFRSPEDFAFLADARTAVPGG 64
DB 17 TSFVATDNTDSSIVYLAEEQVLGCPDVSALQLLSNFEAVFDAPDD--FYSDAKVL--- 71
QY 65 GGGGDLRVHRCVLSARSPLRGVFAARRAAAAGGGEDGSERLRELLGGGEEVEVG 124
DB 72 -SDGREVFHRCVLSARSFESKALA--AAKKEKDSNNTAAVKLEKEI----AKDVEVG 124
QY 125 YEALRLVLDYLSGRVGLPKAACLCVDEDCAHVGHCPAVAFMAQVLFRASTFQVAELTN 184
DB 125 FDSVTVLAYVYSSRVPPKGVSECADENCCHVACRPVDFMLEVLYLAFIEKIPELIT 184
QY 185 LFQRLLDVLDKVDNLLILLISVANLCNCKSMKLLRCLDMVRSNLDMLTLEKSLPPD 244
DB 185 LYQRHLDDVVDKVVIVTLVILKIANICGKACMKLLDRCKEIIIVKSNVDMVLSLESLPEE 244
QY 245 VIKQIDARLSGLISPENKGFPMKRVHRIHRALSDSDVELVRLMLITEGOTNLDADAFALH 304
DB 245 LVKEIIDRKEGLVEVPKV---KHVSNNVHKALSDSDIELVKLLKEDHTNLDACALH 300
QY 305 YAVEHCDSKITTELDLADLVNHRNPRGYTLVHIAARRPEKTIIVSLTKGARPADVTF 364
DB 301 FAVAYCNVKTATDLKLDLVNHRNPRGYTLVHVAARRKEPQILSLLEKGSASATL 360
QY 365 DGRVAQVSKRLTKGDFYGVTEGKPSPKDRLCIELEQAERDPPQLGSEASVSLAMAGE 424
DB 361 EORTALMTAKQATWAVECANNIPEOCKKSLKGLRCVLEIQEDKREQIPROVPPSFAVAAD 420

QY 425 SLRGRLLYLENRVALARIMFPMEARVAMDAOVDGTFLENLGSGANPPPP---QRTTV 480
DB 421 ELKMTLLDLENRVLAQRLLFPTPEAQAARMAEIAEMKGTCEFIYTS---LEPDRLTGTKRTSP 477
QY 481 DLNESPFIKKEEHLARMTALSKTVELGKRFPRCSNVLDKIMD-DETPVSVSLGRDTSAEK 539
DB 478 GYKIAFRILEEHQSRKALKSKTVELGKRFPRCSAVLDQIMNCEDLTQLACGEDDTAEK 537
QY 540 R----KRFHDLQDVLOKAFHEDEKENDRSGLSSSSSTS 574
DB 538 RLOKQRYMEIQETLKAFSEDNELGNLSLDTDSSTS 576
RESULT 5
US-08-996-685-8
Sequence 8, Application US/08996685
Patent No. 6031153
GENERAL INFORMATION:
APPLICANT: Ryals, John
APPLICANT: Friedrich, Leslie
APPLICANT: Uknes, Scott
APPLICANT: Molina, Antonio
APPLICANT: Ruess, Wilhelm
APPLICANT: Knauf-Beiter, Gertrude
APPLICANT: Kessmann, Helmut
APPLICANT: Oostendorp, Michael
TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6031153artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6031153th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/996,685
FILING DATE: 27-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION DATA: US 08/761,543
FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA: US 60/034,378
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA: US 60/035,022
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA: US 60/035,024
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA: US 08/875,015
FILING DATE: 16-JUL-1997

ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-996-685-8

Query Match 43.0%; Score 1270; DB 3; Length 593;
Best Local Similarity 47.0%; Pred. No. 4.6e-121;
Matches 272; Conservative 113; Mismatches 166; Indels 28; Gaps 9;

QY 5 TSHVTNFAFSDSDSASVEEGDADADVEALRLSDNLAARFSPEDFAFLADARIAVPGG 64
Db. 17 TSFVATDNTDSSIVYLAQAQVLTGPDVSALQLLSNFESVFDPDD--FYSDAKVL--- 71
QY 65 GGGGGLRVHRCVLSARSFPLRGVFAARRAAAAGGGGDSERLELRLLGGGEEVEVG 124
Db. 72 -SDGREVSFRCVLSARSFFKSALA--AAKKEKDSNNTAAVKLEKEI----AKDYEVG 124
QY 125 YEALRLVLDYLYSGRVGDLPLKACICVDECAHVGHCPAVAFMAQVLFPAASTFOVAELTN 184
Db. 125 FDSVTVLAIVYSSRRVPPKPGVSECADENCCHVACRPVDFMLEVLYLAFIKIPELIT 184
QY 185 LFQRLDLDVLDKVEVDNLLILSVANLCNCKMCKLLERCLDMVRSNLDMLTLEKSLPPD 244
Db. 185 LYQRHLDDVVDKVIETDVLILKLANICGKACMKLLDRCKEIIIVSNVDMVLSLEKSLPEE 244
QY 245 VIKQIIDARLSGLISPNKGFPPKHVRRIHRLALSDDDVELVRLMLTTEGOTNLDDAFALH 304
Db. 245 LVKEIIDRRKELGLEVPKVK---KHVSNVHKALSDDDIELVKLLKEDHTNLDACALH 300
QY 305 YAVEHCDSKITTELDLALADVNNHPRGYTVLHIAARREPKIIVSLITKGARPADVTF 364
Db. 301 FAVAYCNVATDLDLADVNNHPRGYTVLHVAAMKEPQLILSLLEKSGASAEATL 360
QY 365 DGRKAVOISKTLKQDYGTVGTEEGKPSKDRCLCIILEQAERDPOLGEASVSLAMAGE 424
Db. 361 EGRALMIKQATMAVECNIPQCKHSLKGLRCVLEIQEDKREQIPRDVPPSFVAAD 420
QY 425 SLRGLLYLENVALARIMFPMEARVAMDIAQVDGTLFNLGSGANPPPP---ORTTV 480
Db. 421 ELKMTLLENVALAQLRPTEAQAAMEIAEMKGTCEFTVTS---LEPDRLTGKRTSP 477
QY 481 DLNESFFIMKEEHARMTALSKTVLKGKFFPPRCNSVNLKIND-DTDPVSLGRDTSAEK 539
Db. 478 GVKIAPFRLEEHQSLKSLKSKTVLKGKFFPPRCNSAVLDQIMNCELDTLQACGEDTAEK 537
QY 540 R---KRFHDQVLOKAFHEKDEKNDKRSSSSSSTS 574
Db. 538 RLQKORYMEIQETLKAQFSEDNLELGNLSLTDSTSTS 576

RESULT 6
US-08-989-478-12
Sequence 12, Application US/08989478
Patent No. 5986082
GENERAL INFORMATION:
APPLICANT: Utnes, Scott
APPLICANT: Hunt, Michelle
APPLICANT: Steiner, Henry-York
APPLICANT: Ryals, John
TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5986082artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 5986082th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,478
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 521 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-989-478-12

Query Match 40.3%; Score 1188.5; DB 2; Length 521;
Best Local Similarity 48.0%; Pred. No. 7.9e-113;
Matches 251; Conservative 100; Mismatches 149; Indels 23; Gaps 7;
QY 5 TSHVTNFAFSDSDSASVEEGDADADVEALRLSDNLAARFSPEDFAFLADARIAVPGG 64
Db. 17 TSFVATDNTDSSIVYLAQAQVLTGPDVSALQLLSNFESVFDPDD--FYSDAKVL--- 71
QY 65 GGGGGLRVHRCVLSARSFPLRGVFAARRAAAAGGGGDSERLELRLLGGGEEVEVG 124
Db. 72 -SDGREVSFRCVLSARSFFKSALA--AAKKEKDSNNTAAVKLEKEI----AKDYEVG 124
QY 125 YEALRLVLDYLYSGRVGDLPLKACICVDECAHVGHCPAVAFMAQVLFPAASTFOVAELTN 184
Db. 125 FDSVTVLAIVYSSRRVPPKPGVSECADENCCHVACRPVDFMLEVLYLAFIKIPELIT 184
QY 185 LFQRLDLDVLDKVEVDNLLILSVANLCNCKMCKLLERCLDMVRSNLDMLTLEKSLPPD 244
Db. 185 LYQRHLDDVVDKVIETDVLILKLANICGKACMKLLDRCKEIIIVSNVDMVLSLEKSLPEE 244
QY 245 VIKQIIDARLSGLISPNKGFPPKHVRRIHRLALSDDDVELVRLMLTTEGOTNLDDAFALH 304
Db. 245 LVKEIIDRRKELGLEVPKVK---KHVSNVHKALSDDDIELVKLLKEDHTNLDACALH 300

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Query Match      40.3%   Score 1188.5; DB 3;   Length 521;
Best Local Similarity 48.0%; Pred. No. 7.9e-113;
Matches 251; Conservative 100; Mismatches 149; Indels 23; Gaps 7;

QY  5  TSHVTNAFSDSOSASVEGDGDADADADVEALRRLSDNLNAAAFSPDEQFAFLADARIAPGG 64
Db   11  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  17  TSPVATDNTDSSIVYLAAPQVLTPGDSALQSLNSFESVDFSDPD---FYSDAKIVL--- 71
Db   11  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  65  GGSGGDLRVHRCVLSARGPFLRGVFARRAAAGGGGEGDSERLERELGGGGEVEVG 124
Db   11  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  72  -SDGREVSFHRVCVLSARSSFFKSALA--AAKKEKDSNNTAAVKLEKEI----AKDYEVG 124
Db   11  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  125 YEALRLVLVDLYLSGRVGDLPKAACLCYDDECAHNGCHPAPVAFMAQVLFPAASTQVLAELTN 184
Db   11  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  125 FDSVVTVLAVYSSRVRRPPKGVSCADENGCHVACRPAPVDFMLEVLYLAFIKPELIT 184
Db   11  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  185 LFQRRLLDVLDKVEVDNLLILLSVANICNCKSCMKLLERLDWMVYRSLNDMITLEKSLPPD 244
Db   11  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  185 LYORHLDDVVYKVVIEDTILILKLANICGKACMKLLDKCKEIIIVKSNVDMVLSLESLPEE 244
Db   11  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  245 VIKQIDARLSGLISPENKGPFPKPHVRIHRALDSDSDVELVRLMLLTGGOTNLDLDAFALH 304
Db   11  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  245 LVKEIIDRRKELGLEVPKYK---KHVSNVHKALSDDDIELVLLKLLKEDHTNLDACALH 300
Db   11  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  305 YAVEHCSKTTTELDDALADVNHNRNPRGYTVLHTAARRPEPKIIVSLTKGARPADVTF 364
Db   11  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  301 FAVAYCNVKTATDLKLDLADVNHNRNPRGYTVLHVAAARKPEQLTLLSLEKGASASRTL 360
Db   11  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  365 DGRKAVOISKRLLQKQGYGVTEEGKSPKDRCLTEILQEAKERDPQIGEASVSFLAMAGE 424
Db   11  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  361 EGRALMIAKQATMAVECNINPEQCKHSLKRLCVLEILLEQDEKREQIPDRVPPPSFAVAAD 420
Db   11  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  425 SLRGLRLYLENRVALARINFPMEARVAMIDIAQVDTGLEFNLGSGANPPPER-----QRTTV 480
Db   11  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  421 ELKMTLLDENRVVALAQRLFPTEAQAAEMIAEMKGTCEFIVTS---LEPDLRTGKTGRTSP 477
Db   11  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  481 DLNPSFTPMKEHIAUWALSKTVELGKRFPPRCNSVNLDXKIND 523
Db   11  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  478 GVKIAPFLIEEHQSRLKALSKTVELGKRFPPRCNSAVLDQIMN 520
Db   11  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT      8
US-08-989-478-10
; Sequence 10, Application US/08989478
; Patent No. 5986082
; GENERAL INFORMATION:
; APPLICANT: Uknes, Scott
; APPLICANT: Hunt, Michelle
; APPLICANT: Steiner, Henry-York
; APPLICANT: Ryals, John
; TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
; TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
; NUMBER OF SEQUENCES: 32

```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: No. 5986082artis Corporation
;; STREET: 3054 Cornwallis Road
;; CITY: Research Triangle Park
;; STATE: No. 5986082th Carolina
;; COUNTRY: USA
;; ZIP: 27709
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/989,478
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/033,177
;; FILING DATE: 13-DEC-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/034,379
;; FILING DATE: 27-DEC-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/034,382
;; FILING DATE: 27-DEC-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/034,730
;; FILING DATE: 10-JAN-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/035,021
;; FILING DATE: 10-JAN-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/035,022
;; FILING DATE: 10-JAN-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Melgs, J. Timothy
;; REGISTRATION NUMBER: 38,241
;; REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (919) 541-8587
;; TELEFAX: (919) 541-8689
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 469 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-989-478-10

Query Match 38.4%; Score 1134; DB 2: Length 469;
Best Local Similarity 51.4%; Pred. No. 2.5e-107;
Matches 233; Conservative 89; Mismatches 115; Indels 16; Gaps 5;

QY 131 VLIDYXSGRVDLPKAAACLVDEDCAHVGHCPAVAFMAQVLAASFOVAELNLFQRL 190
Db 7 VLAVYSSRVPPKGVSECADENCCVACRPAYDFMVLVLAIFKIPILITLQRLH 66
QY 191 LDVLDKVEVDNLLILSVANLCNCKMLERCLDMVRSNLDMLTLEKSLPPDVIKQII 250
Db 67 LDVVQKVVIEDTLVLKLANICGKACMLDRCKEIIKVSNDVMVSLKSLPEELVKRI 126
QY 251 DARLSGLISPNKGNPKHVRIRHRLSDSDVELVRLMLTEGQTNLDDAFALHAYEHC 310
Db 127 DRKELGLEVPKVK----KHVSNVHKAISDDIELVKLLKEDHTNDDACALHFAVAYC 182
QY 311 DSKITTELLDLADVNNHPRGTYVLHIAARRRPEKIIIVSLTKGARPAVDVTFDGRKAV 370
Db 183 NVATDALLKLDADVNNHPRGTYVLHVAARKPEQLIILSLLEKASASEATLEGTAL 242
QY 371 QISKRLTKQDVTGVTVEEGKSPKDRLCIEILFEQARRDPQOLGEASVSLAMAGESLRGL 430
Db 243 MIAKQATMAVECNIPQCKHSLKGLRCVLEIQEDKREQIPRDVPPSFAVADELKMTL 302

QY 431 LYLENVALARIMFPEARVAMDIQVGTLEFNLSGANPPPP---ORTTVDLNESP 486
Db 303 LDLENVALAQRLEFTEAQAAMEIAEMKGTCEIVTS---LEPDRLTGKRTSPGVKIAP 359
QY 487 FIMKEEHLARMTALSKTVELGKRRFFRCNSNVLDKIMD-DETDVPVSLGRDTSABKR---K 541
Db 360 FRILEEHQSRKALSKTVELGKRRFFRCNSAVLDQINNCEDLTQACGEDDTAEKRLQKKQ 419
QY 542 RFHDLQDVLOKAFHEDKEENDRSGLSSSSSSSTS 574
Db 420 RYMEIQETLKKAFSEDNLELGNLSLTDSTSTS 452

RESULT 9
US-08-996-685-10
; Sequence 10, Application US/08996685
; Patent No. 6031153
; GENERAL INFORMATION:
; APPLICANT: Rvals, John
; APPLICANT: Friedrich, Leslie
; APPLICANT: Uknes, Scott
; APPLICANT: Molina, Antonio
; APPLICANT: Ruess, Wilhelm
; APPLICANT: Knauf-Beiter, Gertrude
; APPLICANT: Kung, Ruth
; APPLICANT: Kessmann, Helmut
; APPLICANT: Oostendorp, Michael
; TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6031153artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6031153th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,685
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/761,543
; FILING DATE: 6-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,378
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,379
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,382
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,730
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,021
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,022
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,024
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/875,015
; FILING DATE: 16-JUL-1997

ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21215/PL/CGC1912
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 469 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-996-685-10

Query Match 38.4%; Score 1134; DB 3; Length 469;
Best Local Similarity 51.4%; Pred. No. 2.5e-107;
Matches 233; Conservative 89; Mismatches 115; Indels 16; Gaps 5;
QY 131 VLDYLYSGRVGDLPRACACLVDEDCAHVGHCHPAVAFMAQVLFPAASTFOVAELTNLFQRRL 190
Db 7 VLAYVYSSRVPPKGVSECADENCHVACRPVDFMFLVLYLAFIFKIPELITLYQRHL 66
QY 191 LDVLDKVEVDNLLILSVANLCKNCKMLERCLDMVYRSNLDMTITLKSLLPDPVIRKII 250
Db 67 LDVVDKVVIEDTLVILKLANICGKACMKLLDRCKEIIIVKSNVDVMSLEKSLPEELVKEII 126
QY 251 DARLSGLISPENKGFPPKRVHRIHRLDSDVVELVRMLLTGEGTNLDDAFALHYAVEHC 310
Db 127 DRKELGLEVPVKV---KHVSNVHKAALDSDIELVKLLKEDHTNLDACALHFAVAYC 182
QY 311 DSKITTELDDALADVNHRNPRGYTVLHIAARRPKIIVSLTLLTGKARPADVTDFGRKAV 370
Db 183 NVKATDILLKDLADVNHRNPRGYTVLHVAARKPEQILSLLEKGSASEATLEGRAL 242
QY 371 QISKRLTKOGDYFGVTEGKPSKDLCEILEQAEERDPQOLGEASVSLAMAGESLGRRL 430
Db 243 MIAKQATMAVECNNIPEQCKHSLKGLRCLVEILEQEDKREQIPRDVPPSPFAVADELKMTL 302
QY 431 LYLENRVALARIMFPMEARVAMDIQVDTGLEFNLGSGANPPPER---QRTVDLINESP 486
Db 303 LDLENRVALAQRLEFTEAQAAMEIAEMKGTCEFIVTS---LEPDRLTGKRTSPGVKIAP 359
QY 487 FIMKEEHLARMTALSKTVELGKRRFPPRCNSVLDKIMD-DETDPVSLGRDTSAEKR---K 541
Db 360 FRILEEHQSRKALKSKTVELGKRRFPPRCNSAVLDQIMNCDLTOLACGEDDTAEKRLQKKQ 419
QY 542 RFHDLQVLQAKFHEKDEKNDKSLSSSSSTS 574
Db 420 RYMEIQETLAKAFSEDNLEGLNLSLTDSTSTS 452

RESULT 10
US-08-989-478-14
Sequence 14, Application US/08989478
Patent No. 5986082
GENERAL INFORMATION:
APPLICANT: Ukes, Scott
APPLICANT: Hunt, Michelle
APPLICANT: Steiner, Henry-York
APPLICANT: Ryals, John
TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5986082artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 5986082th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,478
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21214/PL/CGC1911
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 397 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-989-478-14

Query Match 35.7%; Score 1052.5; DB 2; Length 397;
Best Local Similarity 53.4%; Pred. No. 4e-99;
Matches 212; Conservative 76; Mismatches 98; Indels 11; Gaps 3;
QY 131 VLDYLYSGRVGDLPRACACLVDEDCAHVGHCHPAVAFMAQVLFPAASTFOVAELTNLFQRRL 190
Db 7 VLAYVYSSRVPPKGVSECADENCHVACRPVDFMFLVLYLAFIFKIPELITLYQRHL 66
QY 191 LDVLDKVEVDNLLILSVANLCKNCKMLERCLDMVYRSNLDMTITLKSLLPDPVIRKII 250
Db 67 LDVVDKVVIEDTLVILKLANICGKACMKLLDRCKEIIIVKSNVDVMSLEKSLPEELVKEII 126
QY 251 DARLSGLISPENKGFPPKRVHRIHRLDSDVVELVRMLLTGEGTNLDDAFALHYAVEHC 310
Db 127 DRKELGLEVPVKV---KHVSNVHKAALDSDIELVKLLKEDHTNLDACALHFAVAYC 182
QY 311 DSKITTELDDALADVNHRNPRGYTVLHIAARRPKIIVSLTLLTGKARPADVTDFGRKAV 370
Db 183 NVKATDILLKDLADVNHRNPRGYTVLHVAARKPEQILSLLEKGSASEATLEGRAL 242
QY 371 QISKRLTKOGDYFGVTEGKPSKDLCEILEQAEERDPQOLGEASVSLAMAGESLGRRL 430
Db 243 MIAKQATMAVECNNIPEQCKHSLKGLRCLVEILEQEDKREQIPRDVPPSPFAVADELKMTL 302
QY 431 LYLENRVALARIMFPMEARVAMDIQVDTGLEFNLGSGANPPPER---QRTVDLINESP 486
Db 303 LDLENRVALAQRLEFTEAQAAMEIAEMKGTCEFIVTS---LEPDRLTGKRTSPGVKIAP 359
QY 487 FIMKEEHLARMTALSKTVELGKRRFPPRCNSVLDKIMD 523
Db 360 FRILEEHQSRKALKSKTVELGKRRFPPRCNSAVLDQIMN 396

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RESULT 11
US-08-996-685-14
; Sequence 14, Application US/08996685
; Patent No. 6031153
; GENERAL INFORMATION:
; APPLICANT: Rvals, John
; APPLICANT: Friedrich, Leslie
; APPLICANT: Uknes, Scott
; APPLICANT: Molina, Antonio
; APPLICANT: Russ, Wilhelm
; APPLICANT: Knauf-Beiter, Gertrude
; APPLICANT: Kung, Ruth
; APPLICANT: Kessmann, Helmut
; APPLICANT: Ostendorf, Michael
; TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 6031153artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6031153th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,685
; FILING DATE:
; CLASSIFICATION:
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; FILING DATE: 6-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,378
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; APPLICATION NUMBER: US 60/034,379
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,382
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,730
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,021
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,022
; FILING DATE: 16-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,024
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/875,015
; FILING DATE: 16-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Melgs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-21215/PI/CGC1912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
; US-08-996-685-14
Query Match 35.7%; Score 1052.5; DB 3; Length 397;
Best Local Similarity 53.4%; Pred. No. 4e-99;
Matches 212; Conservative 76; Mismatches 98; Indels 11; Gaps 3;
QY 131 VLDYLYSGRVGDLPKAACLCVDEDCAHVGHCPAVAFNAQVLAFAASTFQVAELTNLFORRL 190
Db 7 VLAYVYSSRVPPPKGVSECADENCCHVACRPADVMEVLVLAIFPKIPELITLYORHL 66
QY 191 LDVLDKVEVDNLLILSVANLCKNSCKMLERCIDMVRSNLDMLTLEKSLPPDVIKQII 250
Db 67 LDVVDKVVIEDTLVILKLANICGKACMKLLDRCKEIIIVKSNVDMVSEKSLPEELVKEII 126
QY 251 DARLSGLISPENKGPKNKHVRIRHRALEDSDVELVPMLEGTOTNDDAFALHYAVEHC 310
Db 127 DRKELGLEVPKVK---KHVSNVHRAKALSDDIELVKLLKEDHTNDDACALHFAVAYC 182
QY 311 DSKITTELDLADLVNHRNPRGYTVLHIAARRPEKIIIVSLTKGARPADVTDFGRKAV 370
Db 183 NVKATDLDLADLVNHRNPRGYTVLHVAAMRKEPOLILSLLEKGSASEATLEGRAL 242
QY 371 QISKRLTKOGDYFGVTEEGKPSKDRLCIELEQAEORRDPQLGEASVSLAMAGESLRGL 430
Db 243 MIAQATMAVECNIPQCKHSLKGLCVLEIQEDKREQIPRDVPPSFAVADELKWTLL 302
QY 431 LYLENRVALARIMFPMEARVAMDIQAQVDGTLEFNILGSGANPPPP---QRTTVDLNESP 486
Db 303 LDLENRVALAQLFPTEAQAAMEIAEMKGTCEFTVTS---LEPDRLTGTRKTSFGVKIAP 359
QY 487 FIMKEEHLARMTALSKTVELGKRFPPRCNSVLDKIMD 523
Db 360 FRILEEHQSRKALSKTVELGKRFPPRCNSAVLDQIMN 396
RESULT 12
US-08-989-478-16
; Sequence 16, Application US/08989478
; Patent No. 5986082
; GENERAL INFORMATION:
; APPLICANT: Uknes, Scott
; APPLICANT: Hunt, Michelle
; APPLICANT: Steiner, Henry-York
; APPLICANT: Ryals, John
; TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5986082artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 5986082th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,177
; FILING DATE: 13-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,379
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,382

```

ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,685
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/761,543
FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,378
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,024
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/875,015
FILING DATE: 16-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGCI1912
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-996-685-16

Query Match 25.4%; Score 751; DB 2; Length 261;
Best Local Similarity 54.6%; Pred. No. 1.3e-68;
Matches 142; Conservative 54; Mismatches 56; Indels 8; Gaps 2;
QY 107 RLELRELLGGGEEVGEYALRLVLDLYSGRVGDLKPAACLCVDEDCAHVGHCPAVAF 166
Db 10 KLEKEI----AKDYEVGDSVTVLAYVSSRPPKGVSECAENCCCHVACRPVDF 65
QY 167 MAQVLFASFTFOVAELTNLFORRLDVLQKVEVDNLLILSVANLCNCKMKLLERCLDM 226
Db 66 MLEVLYLAFIKPIPELITLYQRHLLDVQVVKVIEDTLVILKLANICGKACMKLLDRCKEI 125
QY 227 VVRSNLDMTLEKSLPPDVIKQIIDARLSGLISPENKGFNKHVRRTHRALDSDDELV 286
Db 126 IVKSNVDMSLEKSLPEELVKIIDRRKELGLEVPVKV----KHVSNVHKALDSDDELV 181
QY 287 RMLLTGQTNLDDAFALHYAVEHCDSKITTELLDLALADVNHRNPRGYTVLHIAARRREP 346
Db 182 KLLKEDHTNLDACALHFAVACNVKTATDLKLLDLADVNHRNPRGYTVLHVAAMRKEP 241
QY 347 KIIVSLTKCARPDVTFDG 366
Db 242 QLILSLLEKGASAEATLEG 261

US-08-996-685-16
Query Match 25.4%; Score 751; DB 3; Length 261;
Best Local Similarity 54.6%; Pred. No. 1.3e-68;
Matches 142; Conservative 54; Mismatches 56; Indels 8; Gaps 2;
QY 107 RLELRELLGGGEEVGEYALRLVLDLYSGRVGDLKPAACLCVDEDCAHVGHCPAVAF 166
Db 10 KLEKEI----AKDYEVGDSVTVLAYVSSRPPKGVSECAENCCCHVACRPVDF 65
QY 167 MAQVLFASFTFOVAELTNLFORRLDVLQKVEVDNLLILSVANLCNCKMKLLERCLDM 226
Db 66 MLEVLYLAFIKPIPELITLYQRHLLDVQVVKVIEDTLVILKLANICGKACMKLLDRCKEI 125
QY 227 VVRSNLDMTLEKSLPPDVIKQIIDARLSGLISPENKGFNKHVRRTHRALDSDDELV 286
Db 126 IVKSNVDMSLEKSLPEELVKIIDRRKELGLEVPVKV----KHVSNVHKALDSDDELV 181
QY 287 RMLLTGQTNLDDAFALHYAVEHCDSKITTELLDLALADVNHRNPRGYTVLHIAARRREP 346
Db 182 KLLKEDHTNLDACALHFAVACNVKTATDLKLLDLADVNHRNPRGYTVLHVAAMRKEP 241

RESULT 13
US-08-996-685-16
Sequence 16, Application US/08996685
Patent No. 6031153
GENERAL INFORMATION:
APPLICANT: Ryals, John
APPLICANT: Friedrich, Leslie
APPLICANT: Uknes, Scott
APPLICANT: Molina, Antonio
APPLICANT: Ruess, Wilhelm
APPLICANT: Knauf-Beiter, Gertrude
APPLICANT: Kung, Ruth
APPLICANT: Kessmann, Helmut
APPLICANT: Oostendorp, Michael
TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6031153artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NO. 6031153th Carolina
COUNTRY: USA

QY 347 KIIVSLTGTGADPVDFTG 366
Db 242 QLILSLLEKGAASEATLEG 261

RESULT 14

US-09-082-059-2
; Sequence 2, Application US/09082059A
; Patent No. 6225086
; GENERAL INFORMATION:
; APPLICANT: Morrow, Jon S.
; TITLE OF INVENTION: No. 6225086el Ankyrin Proteins and a Method for Their Identification
; FILE REFERENCE: 44574-5002-US
; CURRENT APPLICATION NUMBER: US/09/082,059A
; CURRENT FILING DATE: 1998-05-21
; EARLIER APPLICATION NUMBER: 60/047356
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1088
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-082-059-2

Query Match 4.5%; Score 133; DB 4; Length 1088;
Best Local Similarity 24.6%; Pred. No. 0.00021;
Matches 66; Conservative 43; Mismatches 107; Indels 52; Gaps 12;

QY 254 LSLGLISPENKGPKNH-VRRIRHALSDDDVELVRMLTTEG-----QTNLDDAFALHYAV 307
Db 301 VSLLRGNANVNSKSGTPLHLAQEDRVNVAEVLVNGAHVDAQTKMGYT-PLHVGC 359
QY 308 EHCDSKITTELLDALADVNNRPNRGYTVLHIAARREPKIIVSLTGTGADPVDFTDGR 367
Db 360 HYGNIKIVNELLQHS-AKYNNAKTNGYTPHQAQQGHTHIINVLQNNASPNELIVNGN 418
QY 368 KAVQISKRITKQGDYGVTEEGSPKDR-L-CIEILEQARRDPQLGASVSL-----419
Db 419 TALGIARRL-----GYISVVDTLKIVTEETMTTTEKHKMNVPTMNEVLDMSDDEGED 474
QY 420 AMAGESLRGLLYENRVALRIMFPEAR-VAMDTAQVDGTLEENLGSGANPPPERQRT 478
Db 475 AMTGD-----DKYLGPDUKELGDDSLPAEGYMGFSL--GARSASDRSYT 518
QY 479 TVDLNESPT-----MKEEHL 494
Db 519 ---LNRSSYARDSMTEELLVPSKEQHL 543

RESULT 15

US-09-172-977-4
; Sequence 4, Application US/09172977
; Patent No. 5989863
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Yue, Henry
; TITLE OF INVENTION: HUMAN ANKYRIN FAMILY PROTEIN
; FILE REFERENCE: PF-0615 US
; CURRENT APPLICATION NUMBER: US/09/172,977
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 1839
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: g29491

US-09-172-977-4

Query Match 4.3%; Score 127; DB 2; Length 1839;
Best Local Similarity 21.1%; Pred. No. 0.002;
Matches 81; Conservative 44; Mismatches 130; Indels 128; Gaps 14;

QY 69 GDLRVHRCVLSARSPLRGVFARRAAAAGGGGDSERLELELLGGGEEVEVGEAL 128
Db 475 GQVEVYRCLL-----RNGALVDARAREEQTPHIASRLG-----KTEIV 513
QY 129 RLVDLYL-----YSGRVGDLPLKAAACLVDEDCAH-----VGCHPAVA 165
Db 514 QLLLOHMAHPDAATTNGYTPHLISAREGQVDVASVL-LEAGAAHSLATKKGFTPLHVAAK 572
QY 166 FMAQVILFAASTFOVAELTNLFQRRLDVLVDKVEVDNLLLSVANLCNCKMCLLERCLD 225
Db 573 Y-----GSLDVAKL--LLQRR--AADSAGKNGLTPLHVAHYDNQKVALLL-----615
QY 226 MMYRSNLDMTLEKSLPPDVI-----KQIIDARLSLGLISPENKGPKNK 269
Db 616 -----LEKGASPHATAKNGYTPHLIAAKKNOMQIASTLLNYG---AETNIVTKQ 661
QY 270 HVRRIRHALSDDDVELVRMLTTEG-----QTNLDDAFALHYAVE 308
Db 662 GVTPLHLASQEGHTDMVTLLLDKGANIHMSTKSGTSLHLAAQEDKYNVADILTKHGADQ 721
QY 309 HCDSKI-----TTELLDLAL---ADVNNRPNRGYTVLHIAARREPKIIVSL 353
Db 722 DAHTKLGTYTPIIVACHYGNVKNVFNLLKQGANVNAKTNGYTPHQAQQGHTHIINVL 781
QY 354 TKGARPADVTFCGRKAVQISKRL 376
Db 782 QHGAKPNATTANGNTALATAKRL 804

Search completed: July 12, 2001, 17:13:02
Job time: 24 sec

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	Score	Match	Length			
1	131	4.4	1880	1	ANK1_HUMAN	P16157 homo sapien
2	127	4.3	3924	1	ANK2_HUMAN	P01484 homo sapien
3	123	4.2	906	1	KBP2_CHICK	P98150 gallus gall
4	123	4.2	1862	1	ANK1_MOUSE	Q02357 mus musculu
5	120.5	4.1	984	1	KBF1_CHICK	Q04861 gallus gall
6	119	4.0	1966	1	MYSB_CAEEL	P02566 caenorhabdi
7	116.5	3.9	323	1	ANK1_CHRVI	Q06527 chromatium
8	116.5	3.9	439	1	AKR_ARATY	Q05753 arabidopsi
9	116	3.9	782	1	ZAM_SYNY3	Q45363 synechocyst
10	113.5	3.8	854	1	UN33_CAEEL	Q01630 caenorhabdi
11	112	3.8	832	1	ANK3_HUMAN	P57078 homo sapien
12	111.5	3.8	338	1	TR19_HUMAN	Q15653 homo sapien
13	111.5	3.8	646	1	WEEL_MOUSE	P47810 mus musculu
14	111.5	3.8	971	1	KBF1_MOUSE	P25799 mus musculu
15	111	3.8	744	1	YG4_V_HALSO	P21562 haloferax s
16	110	3.7	411	1	CLPX_HAEIN	P44838 haemophilus
17	110	3.7	418	1	SEP7_HUMAN	Q16181 homo sapien
18	109	3.7	436	1	SEP7_RAT	Q9WVC0 rattus norv
19	108	3.7	969	1	KBF1_HUMAN	P19838 homo sapien
20	107.5	3.6	1964	1	NTC4_MOUSE	P31695 mus musculu
21	107	3.6	570	1	SYG_ARCFU	Q29346 archaeoglob
22	107	3.6	1220	1	DPOL_HSVEB	P28858 equine herp
23	106.5	3.6	2531	1	NTCL_MOUSE	Q01705 mus musculu
24	106	3.6	317	1	MAD3_HUMAN	P25963 homo sapien
25	106	3.6	522	1	KBF1_RAT	Q63369 rattus norv
26	105	3.6	436	1	SEP7_MOUSE	O55131 mus musculu
27	105	3.6	777	1	BAR1_HUMAN	Q99728 homo sapien
28	105	3.6	1094	1	EX5B_MYCTU	P96920 mycobacteri
29	105	3.6	1110	1	CYGD_BOVIN	P55203 bos taurus
30	104.5	3.5	1588	1	AROT_YEAST	P08566 s pentacfunc
31	103.5	3.5	824	1	YOTS_CAEEL	P34651 caenorhabdi
32	103	3.5	610	1	DNK_STAAU	P45554 staphylococ
33	102.5	3.5	998	1	DNK_PTVN3	P30662 pseudorabie

VARIANT HS ILE-462.
 MEDLINE-96225450; PubMed-8640229;
 Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,
 Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A.,
 Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;
 "Ankyrin-1 mutations are a major cause of dominant and recessive
 hereditary spherocytosis";
 Nat. Genet. 13:214-218(1996).
 CC -1- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL
 ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO
 NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE
 CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.
 CC ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE
 CC CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;
 CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC
 CC PLASMA MEMBRANE.
 CC -1- ALTERNATIVE PRODUCTS: VARIOUS ISOFORMS OF ANKYRIN ARE PRODUCED BY
 CC ALTERNATIVE SPLICING. THE SEQUENCE SHOWN IS THAT OF ANKYRIN
 CC VARIANT 2.1.
 CC -1- PTM: REGULATED BY PHOSPHORYLATION.
 CC -1- PTM: ACYLATED BY PALMITIC ACID GROUP(S).
 CC -1- DISEASE: DEFECTS IN ANK1 ARE THE CAUSE OF DOMINANT AND RECESSIVE
 CC HEREDITARY SPHEROCYTOSIS (HS).
 CC -1- SIMILARITY: CONTAINS 23 ANK REPEATS.

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CC EMBL; X16609; CA34610.1; -;
CC EMBL; M28880; AAA51732.1; -;
DR PIR; S08275; SJHUK.
DR PIR; A35049; A35049.
DR HSP; Q00420; IAWC.
DR MIM; I82900; -;
DR InterPro; IPR000488; -;
DR InterPro; IPR000906; -;
DR InterPro; IPR002110; -;
DR Pfam; PF00791; ZU5; 1.
DR Pfam; PF00023; ank; 22.
DR Pfam; PF00531; death; 1.
DR PROSITE; PS50088; ANK_REPEAT; 20.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
KW Phosphorylation; Lipoprotein; Multigene family; Disease mutation;
KW Elliptocytosis; Polymorphism.
FT INIT_MET 0
FT DOMAIN 1 826
FT 89 KDA DOMAIN (ANION EXCHANGE PROTEIN
FT BINDING DOMAIN).
FT 62 KDA DOMAIN (SPECTRIN BINDING
FT DOMAIN).
FT 55 KDA REGULATORY DOMAIN (REGULATES
FT THE BINDING OF ANKYRIN TO SPECTRIN
FT AND THE BAND 3 PROTEIN).
FT ANK 1. 72
FT ANK 2. 105
FT ANK 3. 138
FT ANK 4. 142
FT ANK 5. 171
FT ANK 6. 200
FT ANK 7. 233
FT ANK 8. 266
FT ANK 9. 299
FT ANK 10. 332
FT ANK 11. 365
FT ANK 12. 398
FT ANK 13. 431
FT ANK 14. 464
FT ANK 15. 497
FT ANK 16. 530
FT ANK 17. 563
FT ANK 18. 596
FT ANK 19. 629
FT ANK 20. 662
FT ANK 21. 695
FT ANK 22. 728
FT ANK 23. 761
FT ANK 24. 794
FT DEATH DOMAIN.
FT MISSING (IN ISOFORM 2.2).
FT H -> D (IN ISOFORM 2.2).
FT TVEGPLEDPSLEVDIDYPMKSHOHTSTPNP -> ELRGS
FT GLQDLIEGRKAQIVKASLRGKO (IN A THIRD
FT ISOFORM).
FT R -> T.
FT /FTId=VAR_000595.
FT V -> I (IN HS)
FT /FTId=VAR_000596.
FT R -> H (IN BRUEGGEN).
FT /FTId=VAR_000597.
FT V -> A.
FT /FTId=VAR_000598.
FT D -> E.
FT /FTId=VAR_000599.
FT

FT VARIANT 1391 1391 S -> T.
FT /FTId=VAR_000600.
FT VARIANT 1285 1285 E -> D.
FT /FTId=VAR_000601.
FT VARIANT 1591 1591 D -> N (IN DUESSELDORF).
FT /FTId=VAR_000602.
FT VARIANT 1698 1698 R -> D.
FT /FTId=VAR_000603.
FT CONFLICT 229 229 A -> S (IN REF. 2).
FT CONFLICT 1545 1545 V -> I (IN REF. 2).
SQ SEQUENCE 1880 AA; 206145 MW; 1C5F5E7EFDICD428 CRC64;

Query Match 4.4%; Score 131; DB 1; Length 1880;
Best Local Similarity 23.6%; Pred. No. 0.86;
Matches 75; Conservative 34; Mismatches 103; Indels 106; Gaps 12;

QY 271 VRRIRALSDDDVELVRLMLT-----EGQNLDDAF----- 301
Db 635 VTPLHLAAQEGHAEMVALLLSKQANGNLKSGLTPLHLVAQEGHPVADVLIKHGVMVD 694
QY 302 -----ALHYAVEHCDSKITTELLDALADYVHNRNPRGYTVLHIAARREPKIIVSLL 353
Db 695 ATTRMGVTPPLHVASHYGNIKLVKFLQ-HQADVNAKTGLGYSPLHQAQOGHTDIVTLL 753
QY 354 TKGARPADVTFDGRKAVQISKRLTKQDYGFGVTEEGK-----PSPKDRLCI----- 399
Db 754 KNGASPNVSSDGTTPLAIAKRL---GYISYDVLKVVDTSETSVLVSKHRMSFPETV 809
QY 400 -EILEQAEERDPQOLGEASVSLAMAGESLGRLLYLENRVALARIMFPPEARVAMIDIAQVD 458
Db 810 DEILDVSEDE-----GEEL-----ISFKAERDSRDVDEEK 840
QY 459 GTLEFNLGSGANPPRQRTTVDLNSPFIKKEHLARMTALSKTVELGKRFPRCSNVL 518
Db 841 ELLDF-----VPKLDQVV-----ESPALPRIP-----CAMPETVIRSEEQEQASKEY 883
QY 519 DKIMDDETPVSLGRDYS 536
Db 884 D---EDSLIPSPATETS 898

RESULT 2
ANK2_HUMAN
ID ANK2_HUMAN STANDARD; PRT; 3924 AA.
AC Q01484; Q01485;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID).
GN ANK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain stem;
RX MEDLINE=94075409; PubMed=8253844;
RA Chan W., Kordeli E., Bennett V.;
FT "440-kD ankyrinB: structure of the major developmentally regulated
FT domain and selective localization in unmyelinated axons.";
RL J. Cell Biol. 123:1463-1473(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC TISSUE=Brain stem;
RX MEDLINE=91302466; PubMed=1830053;
RA Otto E., Kunimoto M., McLaughlin T., Bennett V.;
FT "Isolation and characterization of cDNAs encoding human brain
FT ankyrins reveal a family of alternatively spliced genes.";
RL J. Cell Biol. 114:241-253(1991).
RN [3]
RP REVISIONS.

RA Carpentier S.;
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 463-495 FROM N.A.
 RX MEDLINE=92009921; PubMed=1833308;
 RA Tse W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,
 RA Lux S.E., Ward D.C., Forget B.G.;
 RT "Isolation and chromosomal localization of a novel nonerythroid
 ankyrin gene";
 RL Genomics 10:858-866(1991).
 CC -!- FUNCTION: ANKYRINS ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTO-
 SKELETAL ELEMENTS; THEY BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN
 BAND 4.2, TO NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85,
 AND TO THE CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND
 DESMIN. ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO
 THE CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;
 THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
 CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE
 PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL
 CELLS THROUGHOUT THE BRAIN.
 CC -!- PTM: PHOSPHORYLATED AT MULTIPLE SITES BY DIFFERENT PROTEIN KINASES
 AND EACH PHOSPHORYLATION EVENT REGULATES THE PROTEIN'S STRUCTURE
 AND FUNCTION (POTENTIAL).
 CC -!- SIMILARITY: CONTAINS 23 ANK REPEATS.
 CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 DR EMBL; Z26634; CAB42644.1; -;
 DR EMBL; X56957; CAA40278.1; -;
 DR EMBL; X56958; CAA40279.2; -;
 DR EMBL; M37123; AAG2828.1; -;
 DR PIR; S14533; S14533;
 DR PIR; A39643; A39643;
 DR PIR; B39643; B39643;
 DR PIR; S14569; S14569;
 DR HSP; Q00420; IAWC.
 DR MIM; 106410; -;
 DR InterPro; IPR000488; -;
 DR InterPro; IPR000906; -;
 DR InterPro; IPR002110; -;
 DR Pfam; PF00791; ZUS; 1;
 DR Pfam; PF00023; ank; 22;
 DR Pfam; PF00531; death; 1;
 DR PROSITE; PS50088; ANK_REPEAT; 20;
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1;
 DR PROSITE; PS5017; DEATH_DOMAIN; 1;
 KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
 KW Phosphorylation; Multigene family.
 FT REPEAT 63 92
 FT REPEAT 96 125
 FT REPEAT 129 158
 FT REPEAT 162 191
 FT REPEAT 193 220
 FT REPEAT 232 261
 FT REPEAT 265 294
 FT REPEAT 298 327
 FT REPEAT 331 360
 FT REPEAT 364 393
 FT REPEAT 397 426
 FT REPEAT 430 459
 FT REPEAT 463 492
 FT REPEAT 496 525
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 FT REPEAT 562 591
 FT REPEAT 595 624

FT REPEAT 628 657
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 FT REPEAT 694 723
 FT REPEAT 727 756
 FT REPEAT 760 789
 FT REPEAT 793 822
 FT DOMAIN 1773 1950
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 FT REPEAT 1785 1796
 FT REPEAT 1797 1808
 FT REPEAT 1809 1820
 FT REPEAT 1821 1832
 FT REPEAT 1833 1844
 FT REPEAT 1845 1856
 FT REPEAT 1857 1867
 FT REPEAT 1868 1879
 FT REPEAT 1880 1891
 FT REPEAT 1892 1902
 FT REPEAT 1903 1914
 FT REPEAT 1915 1926
 FT REPEAT 1927 1938
 FT REPEAT 1939 1950
 FT DOMAIN 3536 3620
 FT VARSPLIC 1039 1039
 FT VARSPLIC 1444 3528
 FT CONFLICT 475 476
 FT CONFLICT 971 971
 FT CONFLICT 3581 3582
 FT CONFLICT 3586 3586
 SQ SEQUENCE 3924 AA; 430337 MW; 52AC496C48E29D2 CRC64;
 Query Match 4.3%; Score 127; DB 1; Length 3924;
 Best Local Similarity 21.1%; Pred. NO. 4.2; Indels 128; Gaps 14;
 Matches 81; Conservative 44; Mismatches 130;
 QY 69 GDLRVHRCVLSARSPFLRGVFAARRAAAAGGGGEGDSERLLELRLGGGEEVEVGYEAL 128
 DB 475 GQVEVVRCLL-----RNGALVDARAREBOTPLHIASRLG-----KTEIV 513
 QY 129 RLVLVDYL-----YSGRVGDLPKAACLCVDEDAH-----VGCHPAVA 165
 DB 514 QLLQLQHMAHPDAATTNGYTPLHISAREGQVDVASVL-LEAGAAHSLATKKGFTPLHVAAK 572
 QY 166 FMAQVLFPAASTFOVAELTNLFQRLDLVDLKVVDNLLILSVANLCNCKMKLLERCLD 225
 DB 573 Y-----GSLDVAKL--LLQRR--AADSAGKNGLTPLHVAAHYDNOKVALL----- 615
 QY 226 MVVRSNLDMLTLEKSLPPDVI-----KOIIDARLSLGLISPENKGFPPNK 269
 DB 616 -----LEKGASPHATKNGYTPHIAAKKNQMQIASTLLNYG---AETNIVTKQ 661
 QY 270 HVRRIRHALSDDDVLVRMLLLEG-----QTNLDADAFALHAYVE 308
 DB 662 GVTPLHLASQEGHTDMVTLLLDKGANHMTSKGSLTSLHLAAQEDKVNVDILTCKHGADQ 721
 QY 309 HCDSKI-----TTELDLAL---ADVNHRNPRGYTVLHIAARREPKIIVSLL 353
 DB 722 DAHTKLGTYPLIVACHYGNVKNVFNLLKOGANVNAKTNGYTPHQAQOQGHITHINVL 781
 QY 354 TKGARPADVTFDGRKAVQISKRL 376
 DB 782 QHGAKPNATTANGNTALAIKRL 804
 RESULT 3
 KBF2_CHICK
 ID KBF2_CHICK STANDARD; PRT; 906 AA.
 AC P98150;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)

NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P52 SUBUNIT].

ANK 6.

NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

GLY-RICH.

V -> G (IN REF. 2).

S -> F (IN REF. 2).

N -> K (IN REF. 2).

C -> G (IN REF. 2).

R -> SG (IN REF. 2).

R -> A (IN REF. 2).

E -> Q (IN REF. 2).

A -> G (IN REF. 2).

T -> A (IN REF. 2).

VRVP -> SEA (IN REF. 2).

L -> RC (IN REF. 2).

SPILLSPPPPSRNHL -> RPDTELTTPRAGNV (IN REF. 2).

T -> S (IN REF. 2).

Y -> D (IN REF. 2).

T -> D (IN REF. 2).

ASAL -> SVSL (IN REF. 2).

P -> A (IN REF. 2).

R -> A (IN REF. 2).

R -> A (IN REF. 2).

OE0CE20DB4F30E62 CRC64;

99667 MR;

Query Match 4.2%; Score 123; DB 1; Length 906;

Best Local Similarity 19.7%; Pred. No. 1.1;

Matches 105; Conservative 59; Mismatches 199; Indels 170; Gaps 18;

QY 63 GGGGGGDLVRHRCVLSRSPFLRGVFAARRAAAAGGGE---DGSRLRLRELLGGGGE 119

DB 356 GGAGGAGG-----GAGGGNLSFPYSSGLGYNLYSSSPH 391

QY 120 EYEGYEALRLVLYSGRVD---LPKAACLCVDCAHVCH----- 161

DB 392 PVGGYQG--GVQKAAASERDGDQAPTESTYCRELQRRHLCHLWLLARRNAHALDY 449

QY 162 -----PAVAFMAQVLFASFTQ-----VAELNLFQRLLDVLDKVEVDNLLIL 206

DB 450 SVTADPRMLLAVQRHLAASODENGDTPLHLAIHQFQAVI-KQIEVVVIPSQOII--- 505

QY 207 SVANLCKSKMKLLERCLDMVVRNLDMLTLEKSLPPDVVTKQIIDARLSGLISPENKGF 266

DB 506 ---NITNN-----LQOTPLHLAVITKO--POVVOLLEAHANPTLLDRYNSL 548

QY 267 PNKHVRIRHALDSDVVELVRL----- 290

DB 549 -----LHALQAADPEMLRLHLAHLASATPYLLHLPNFOGLLPVHLAVKAKSPACLDL 601

QY 291 -----TEGQTNLDADAPALHAYAEHCDSKITTELLDLADLVNHRNPRGYTVLHIAARR 343

DB 602 LVRKGADVNGVROGGRTPLHLAVEMENLNATHLVKLGANVNSRTFAGNTPHLAAGL 661

QY 344 REPKIVSLTKGAPADVTGGRKAVOISKRLTKQGDYFGVTEGKPSKDRLCIELE 403

DB 662 GSPTLTKLLKAG---ADVQRENDEPVSPSSVRVPSSD-----TDGDFE-----E 703

QY 404 QAERDPPOLGEASYSLAMAGESLGRLLYLENRVALARIMFPMPEARVAMDAQVDTLEF 463

DB 704 QBEQAMELGEPLSPHTPEE-----EQEAGPR-----QRLHALDLTRSQKVRDI 751

QY 464 NIGSG-----ANPPPERQRTTVDLNEPFIKMEHLARMALSKTVELQKR 509

DB 752 LQASQSPPIILSCPPPSRNHLSDTLDAQLQLLNQYSGSGDMWELAKR 804

RESULT 4

ANKL_MOUSE

ID ANKL_MOUSE STANDARD: PRT; 1862 AA.

AC Q02357;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE ANKYRIN 1 (ERYTHROCYTE ANKYRIN).
GN ANK1 OR ANK-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Erythrocyte;
RX MEDLINE=92345717; PubMed=1386265;
RA White R.A., Birkenmeier C.S., Peters L.L., Barker J.E., Lux S.E.;
RT "Murine erythrocyte ankyrin cDNA: highly conserved regions of the
regulatory domain.";
RL Mamm. Genome 3:281-285(1992).
CC -!- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL
ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2. TO
NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE
CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.
CC ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE
CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;
CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC
PLASMA MEMBRANE.
CC -!- PTM: REGULATED BY PHOSPHORYLATION (BY SIMILARITY).
CC -!- PTM: REGULATED BY PALMITIC ACID GROUP(S) (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS 23 ANK REPEATS.
CC -----
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or send an email to license@sib-sib.ch).
CC -----
DR EMBL; M84756; AAA37236.1; -.
DR HSP; 000420; 1AUC.
DR MGD; MGI:88024; Ank1.
DR InterPro; IPR000488; -.
DR InterPro; IPR000906; -.
DR InterPro; IPR002110; -.
DR Pfam; PF00791; ZU5; 1.
DR Pfam; PF00023; ank; 23.
DR Pfam; PF00531; death; 1.
DR PROSITE; PS50088; ANK_REPEAT; 20.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Cytoskeleton; Repeat; ANK repeat; Phosphorylation; Lipoprotein.
KW Cytoskeleton; Repeat; ANK repeat; 89 KDA DOMAIN (ANION EXCHANGE PROTEIN
DOMAIN 1 827
FT DOMAIN 828 1386
FT DOMAIN 1387 1862
FT REPEAT 40 69
FT REPEAT 73 102
FT REPEAT 106 135
FT REPEAT 139 168
FT REPEAT 170 197
FT REPEAT 201 230
FT REPEAT 234 263
FT REPEAT 267 296
FT REPEAT 300 329
FT REPEAT 333 362
FT REPEAT 366 395
FT REPEAT 399 428
FT REPEAT 432 461
FT REPEAT 465 494
FT REPEAT 498 527
FT REPEAT 531 560
FT REPEAT 564 593
FT REPEAT 597 626

FT REPEAT 630 659
FT REPEAT 663 692
FT REPEAT 696 725
FT REPEAT 729 758
FT REPEAT 762 791
FT DOMAIN 1399 1483
SQ SEQUENCE 1862 AA; 204242 MW; AE6B85B5B29001E5 CRC64;

Query Match 4.2%; Score 123; DB 1; Length 1862;
Best Local Similarity 26.3%; Pred. No. 2.9;
Matches 55; Conservative 24; Mismatches 60; Indels 70; Gaps 8;

QY 271 VRIIRALSDSDVVLVRLLT-----EGQNLDDAF----- 301
DB 632 VTPLHLAAEGHTEWVALLLSKQANGNLGNKSLTPLHLVSGEGHVLVADVLLKHGVTVD 691
QY 302 -----ALHYAVEHCDSKITTELDLADLVNHRNPRGYTLVHIAARRRREPKIIIVSLL 353
DB 692 ATTRMGYTPLVHVSAGYGNIKLVKFLIQ-HQADVNAKTKLGYSPLHQAAQGGHTDIVTLL 750
QY 354 TKGARPADYTFDGRKAVQISKRLTKOGDYFGYTEEK-----PSPKDRLCI----- 399
DB 751 KNGASPNVSSNGTTPLAIAKRL---GYISVTVLKVVTDTSVVLVSDKHRMSYPETV 806
QY 400 -EILE-----QAERRDPO-LGE 414
DB 807 DEILDVSEDEGDELVGSKAERDSRDVGE 835

RESULT 5
KBFL_CHICK STANDARD; PRT; 984 AA.
ID KBFL_CHICK
AC Q04861;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT [CONTAINS: NUCLEAR FACTOR NF-
DE KAPPA-B P50 SUBUNIT].
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92260650; PubMed=1533881;
RA Capobianco A.J., Chang D., Mosialos G., Gilmore T.D.;
RT "p105, the NF-kappa B p50 precursor protein, is one of the cellular
RT proteins complexed with the v-rel oncoprotein in transformed chicken
RT spleen cells.";
RL J. Virol. 66:3758-3767(1992).
RP SEQUENCE FROM N.A.
RC TISSUE-Spleen;
RA Ikeda T., Honjo K., Hirota Y., Onodera T.;
RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: P105 IS THE PRECURSOR OF THE P50 SUBUNIT OF THE NUCLEAR
CC FACTOR NF-KAPPA-B, WHICH BINDS TO THE KAPPA-B CONSENSUS SEQUENCE
CC 5'-GGGNNYYCC-3', LOCATED IN THE ENHANCER REGION OF GENES INVOLVED
CC IN IMMUNE RESPONSE AND ACUTE PHASE REACTIONS. THE PRECURSOR
CC PROTEIN ITSELF DOES NOT BIND TO DNA.
CC -!- SUBUNIT: ACTIVE NF-KAPPA-B IS A HETERODIMER OF AN ABOUT 50 KDA
CC DNA-BINDING SUBUNIT AND THE WEAK DNA-BINDING SUBUNIT P65. TWO
CC HETERODIMERS MIGHT FORM A LABILE TETRAMER.
CC -!- SUBCELLULAR LOCATION: NUCLEAR, BUT ALSO FOUND IN THE CYTOPLASM
CC IN AN INACTIVE FORM COMPLEXED TO AN INHIBITOR (I-KAPPA-B).
CC -!- DOMAIN: THE C-TERMINUS OF P105 MIGHT BE INVOLVED IN CYTOPLASMIC
CC RETENTION INHIBITION OF DNA-BINDING BY P50 HOMODIMERS, AND/OR
CC TRANSCRIPTION ACTIVATION.
CC -!- SIMILARITY: BELONGS TO THE REL/DORSAL FAMILY.
CC -!- SIMILARITY: CONTAINS 7 ANK REPEATS.
CC -----

379	QY	QGDYFGVTEEGKFSPKDR-----LCIEILQEARRDPOLGGEASVSLAMAGESL--RGRL	430
750	Db	--PLFDVEEDKDDDDDEGIVGPTTPLDMAANNEVYDIILNGKPYIAAAVSEDLISQGPL	807
431	QY	LYLENRVALARIMFPMEARVAMDIAOVGDTLEFNLSG-----ANPPPERQRTTVDLN	483
808	Db	REL--NESSKQOLYKLLB---TPDPSKNWSTLAEKLGILGLILNNAFQLSPSP--SKTLLDNY	861
484	QY	ESPPFMKEEHLARMTALSKT-----VELGKRFRFPGRCSNVLDKIMD--DETPDPSVLGRDTS	536
862	Db	KISGTCQELIAAFTQMDHTEAIEVIQKALSSQORSQHQEDKKTIEAFPSLSPTSFAKEET	921
537	QY	AERKRFRHDLQDVLQKAFHEDKEENDRSGLSGS	569
922	Db	GE-----LYNHKFQDPPESTCDSGVETS	943

RESULTS

MYSB CAEEL

"The genes sup-7 X and sup-5 III of *C. elegans* suppress amber nonsense mutations via altered transfer RNA.";
 RL Cell 33:575-583(1983).
 CC -!- FUNCTION: MUSCLE CONTRACTION.
 CC -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
 CC -!- SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
 CC -!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
 CC -!- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
 CC -!- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).
 CC -!- MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS IN *C. ELEGANS*.
 CC -!- MISCELLANEOUS: MHC A AND MHC B ARE FOUND EXCLUSIVELY IN THE BODY WALL MUSCLE. THEY CO-ASSEMBLE INTO BODY WALL THICK FILAMENT.
 CC -!- SIMILARITY: THE GLOBULAR HEAD AA SEQUENCE SHOWS A HIGH DEGREE OF SIMILARITY WITH THE GLOBULAR HEAD SEQUENCES OF MUSCLE & NONMUSCULAR HEAVY CHAINS BY CONTRAST THE ROD SEQUENCE IS LESS CONSERVED, BUT

CC THE PERIODICITIES OF HYDROPHOBIC & CHARGED RESIDUES, WHICH DICTATE
CC THE ALPHA-HELICAL COILED-COIL STRUCTURE, ARE CONSERVED.
CC
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CC
DR EMBL; J01050; AAA28124.1; -
DR EMBL; V01494; CAA24738.1; -
DR PIR; A02992; MWKW
DR HSP; P08799; 1MND
DR InterPro; IPR001609; -
DR InterPro; IPR002928; -
DR Pfam; PF01576; Myosin_tail; 1.
DR Pfam; PF00063; myosin_head; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
KW Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
KW ATP-binding; Methylation; Alkylation; Heptad repeat pattern;
KW Multigene family.
FT DOMAIN 1 850 GLOBULAR HEAD (S1).
FT DOMAIN 851 1966 RODLIKE TAIL (S2 AND LMM DOMAINS).
FT DOMAIN 851 1164 ALPHA-HELICAL TAILPIECE (S2).
FT DOMAIN 1165 1966 LIGHT MEROMYOSIN (LMM).
FT DOMAIN 851 1966 COILED COIL (POTENTIAL).
FT NP_BIND 177 184 ATP (BY SIMILARITY).
FT DOMAIN 665 687 ACTIN-BINDING.
FT DOMAIN 769 783 ACTIN-BINDING.
FT MOD_RES 128 128 METHYLATION (TRI-) (POTENTIAL).
FT MOD_RES 705 705 ALKYLATION (SH-1).
FT MOD_RES 715 715 ALKYLATION (SH-2).
FT DOMAIN 1165 1176 HINGE.
FT DOMAIN 1337 1337 E -> R (IN REF. 2).
FT CONFLICT 1880 1880 I -> L (IN REF. 2).
FT SEQUENCE 1966 AA; 225125 MW; B66F0BB2FE27B67F CRC64;
CC
Query Match 4.0%; Score 119; DB 1; Length 1966;
Best Local Similarity 19.8%; Pred. No. 5.6;
Matches 129; Conservative 106; Mismatches 226; Indels 190; Gaps 32;
QY 13 SDSASVVE-----GDA-DADADVE-----AL-----RRLSNDLAAA 44
DB 1419 ANSKNASLEKTSRLSLVDDDDAQVDVERANGVASALEKKQKGFDTIDEWRKTTDDLAEE 1478
QY 45 FRSPEDFAFLADARIAVPGGGGGGDLRVHRCVLSARSPLRGVFARR-AAAAAGGGGE 102
DB 1479 L-----DGAQRDLR-----NTSTDLFRKNAQAEELAEVVEGLRRE 1513
QY 103 DGSERLELREL---LGGGGEV-----EVGYEARLVLDLYSRVGDLPRAACL 149
DB 1514 NKSLSOEIKDLTDLGEGGRSVHEMOKIIRLEIEKEELQHAL-----1556
QY 150 CVDEDAHVGCHPAPAFMAQVLFAASTFOVAELTNLFORLLDLDKVEDNLLLSVA 209
DB 1557 --DEABAALAEESKVLRAQV-----EVSQRSIERKIOE--KEEFEN-----T 1598
QY 210 NLNCKSMKLLERCLDMVYRSLNMDITLESPPDVIKQIIDARLSGLISPENKGFNNK 269
DB 1599 RKNHARALESMQASLETEAKGRAELRIKKLEGD----INLEIATDANKANAD-AOK 1653
QY 270 HVRIHRLDSDDELVELVRLMFTGGTNLDADAFALHYAVHEHCDSKITTELLDLALAD---V 326
DB 1654 NLKRY-----QEQVRELQIQVEEQEQRNGADTREQFENAEKRALTLQSEKELLVANAEE 1708
QY 327 NHRNPRGYTVLHIAARRRREPKEIIVSLITKGARPADVTDFGRKAVQISKRITKQDFGYT 386
DB 1709 RARKQAEYEAADARDQANANAAQVSSLSAKRKLGEIQAIHA-DLDETL---NEYKAAE 1764
QY 387 EEGKPSPKD--RLCIEILQAEERR-----DPOLGEASVSLAMA-GESLRGRLLYL 433

DB 1765 ERSKKAIAIDATRLAEELRQEQSHQVDRLRKCLEQQLKEIQVRLDEAAALKGG-----1820
QY 434 ENRVALARIMFMEARVAMDIQAQVDTGLBFLNGLSGANPPPERQRTTVDLINESPFIMKEEH 493
DB 1821 -----KKVIAKLEQVRLESELDG-----EQRREFODANKN--LGRADR 1857
QY 494 LARMTALSKTVELGKRFPPRCNSNVLDKIMD-----DETDPVSLGRDTSNEKRRF-- 543
DB 1858 --RVRELQFQVDEDKNFERLQDLIDKLOOKLKTOKKQVEEAELA---NLNLOKYKQLT 1912
QY 544 HDLQVLQKAFHEDKEENDRSGLSSSS-----SSTSICAIR-PRR 582
DB 1913 HQLEDAEERA---DQAENSLSKMRSKSRASASVAPGLQSSASAAVRSR 1960
RESULT 7
ANKH_CHRVI
ID ANKH_CHRVI STANDARD; PRT; 323 AA.
AC Q06527;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ANKYRIN HOMOLOG PRECURSOR.
OS Chromatium vinosum.
OC Bacteria; Proteobacteria; gamma subdivision; Chromatiaceae;
OC Allochromatium.
OX NCBI_TaxID=1049;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D / ATCC 17899 / DSM 180;
RX MEDLINE=93300842; PubMed=8390993;
RA Dolata M.M., van Beeumen J.J., Ambler R.P., Meyer T.E.,
RA Cusanovich M.A.;
RT "Nucleotide sequence of the heme subunit of flavocytochrome c from
RT the purple phototrophic bacterium, Chromatium vinosum. A 2.6-kilobase
RT pair DNA fragment contains two multiheme cytochromes, a flavoprotein,
RT and a homolog of human ankyrin."
RL J. Biol. Chem. 268:14426-14431(1993).
CC -!- SIMILARITY: CONTAINS 8 ANK REPEATS.
CC
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CC
DR EMBL; L13419; AAA23315.1; -
DR HSP; Q00420; 1AMC
DR InterPro; IPR002110; -
DR Pfam; PF00023; ank; 8.
DR PROSITE; PS50088; ANK_REPEAT; 7.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW Signal; ANK repeat; Repeat.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 323 ANKYRIN HOMOLOG.
FT REPEAT 31 60 ANK 1.
FT REPEAT 64 93 ANK 2.
FT REPEAT 97 126 ANK 3.
FT REPEAT 130 159 ANK 4.
FT REPEAT 163 192 ANK 5.
FT REPEAT 196 225 ANK 6.
FT REPEAT 229 258 ANK 7.
FT REPEAT 262 291 ANK 8.
SQ SEQUENCE 323 AA; 33453 MW; 3976D34A9BD607DF CRC64;
CC
Query Match 3.9%; Score 116.5; DB-1; Length 323;
Best Local Similarity 27.7%; Pred. No. 0.75;
Matches 72; Conservative 31; Mismatches 108; Indels 49; Gaps 9;

ANR3_HUMAN
ID ANR3_HUMAN STANDARD; PRT; 832 AA.
AC P57078;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE SERINE/THREONINE-PROTEIN KINASE ANKRD3 (EC 2.7.1.-) (ANKYRIN REPEAT
DE DOMAIN PROTEIN 3).
GN ANKRD3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=20289799; PubMed=10830953;
RX Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishi K., Totoki Y., Choi D.-K., Soeda E.,
RA Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudo J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordisiek G., Hornischer K., Brandt P.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
RA Ranser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA Wehmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Lehrach H., Reinhardt R., Yaspo M.-L.;
RT Nature 405:311-319(2000).
RL The DNA sequence of human chromosome 21.";
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -1- SIMILARITY: CONTAINS 10 ANK REPEATS.
CC
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CC
CC EMBL; AP001743; BAA95526.1;
DR PROSITE; P500107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; P500108; PROTEIN_KINASE_ST; 1.
DR PROSITE; P500111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; P50297; ANK_REPEAT_REGION; 1.
DR PROSITE; P50088; ANK_REPEAT; 9.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
KW ANK repeat.
FT DOMAIN 22 286 PROTEIN KINASE.
FT REPEAT 485 514 ANK 1.
FT REPEAT 518 547 ANK 2.
FT REPEAT 551 580 ANK 3.
FT REPEAT 584 613 ANK 4.
FT REPEAT 617 647 ANK 5.
FT REPEAT 651 680 ANK 6.
FT REPEAT 684 713 ANK 7.
FT REPEAT 717 746 ANK 8.
FT REPEAT 750 780 ANK 9.
FT REPEAT 782 811 ANK 10.
FT NP_BIND 28 36 ATP (BY SIMILARITY).
FT BINDING 51 51 ATP (BY SIMILARITY).
FT ACT_SITE 143 143 BY SIMILARITY.
SQ SEQUENCE 832 AA; 91610 MW; 5D8FFFD5F047ECB CRC64;

Query Match 3.8%; Score 112; DB 1; Length 832;
Best Local Similarity 26.2%; Pred. No. 5.2;
Matches 50; Conservative 29; Mismatches 74; Indels 38; Gaps 7;
QY 221 ERLCDMWRNLDIMTLEKSLPDVVKQIDARLSGLISPE-----NKGFFN 268
DB 456 KKLVDIVSG--DTSKMLKILQPDVDLALDGSALLHLAVAGQEACAKWLLNNANFN 513

QY 269 KHVRR-----THRALDSDVVELVRMLTE-----GOTNLDDAFALHVAVEHCDSKITTELD 320
DB 514 LSNRGSTPLHMAVERVRGVVELLARKISVNAKDEQDTALHFAQNGDESTRLLLE 573
QY 321 LALADVNRHPRGVTVLHIAARRRPRKIIVSLTGTGAPADVTFDGRKA----- 369
DB 574 -KNASVNEVDFEGTTPMHVACQHQENIVRILLRRG---VDVSLQGRDAMWLP LHYAAWQG 629
QY 370 -VQISKRLTKQ 379
DB 630 HLPVIVKLLAKQ 640
RESULT 12
TRI9_HUMAN STANDARD; PRT; 338 AA.
ID TRI9_HUMAN Q15653;
AC Q15653;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE THYROID RECEPTOR INTERACTING PROTEIN 9 (TRIP9).
GN TRIP9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95295737; PubMed=7776974;
RL Lee J.W., Choi H.-S., Gyuris J., Brent R., Moore D.D.;
RT "Two classes of proteins dependent on either the presence or absence
RT of thyroid hormone for interaction with the thyroid hormone
RT receptor.";
RL Mol. Endocrinol. 9:243-254(1995).
CC -1- FUNCTION: THYROID RECEPTOR INTERACTING PROTEINS (TRIPS)
CC SPECIFICALLY INTERACT WITH THE LIGAND BINDING DOMAIN OF THE
CC THYROID RECEPTOR (TR). TRIP9 REQUIRES THE PRESENCE OF THYROID
CC HORMONE FOR ITS INTERACTION.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED.
CC -1- SIMILARITY: CONTAINS 5 ANK REPEATS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC
CC EMBL; L40407; AAC41742.1;
DR HSSP; Q00420; IAWC.
DR InterPro; IPR002110;
DR Pfam; PF00023; ank; 5.
DR PROSITE; PS50088; ANK_REPEAT; 4.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW REPEAT; ANK repeat.
FT REPEAT 57 86 ANK 1.
FT REPEAT 93 122 ANK 2.
FT REPEAT 126 155 ANK 3.
FT REPEAT 206 235 ANK 4.
FT REPEAT 240 269 ANK 5.
FT DOMAIN 186 195 ASP/GLU-RICH (ACIDIC).
SQ SEQUENCE 338 AA; 35514 MW; EA343762D646FB8E CRC64;

Query Match 3.8%; Score 111.5; DB 1; Length 338;
Best Local Similarity 21.3%; Pred. No. 1.7;
Matches 85; Conservative 35; Mismatches 126; Indels 153; Gaps 16;
QY 60 AVPGGGGGG-----GDLRVHRCVLSARSPFLRGVFAARRAAAGG 99
DB 29 AAPGGGGLGAEIGPGLSWAPLVFGVYVTDGDTALHLAVIHQHEPFLDFLL----- 78

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7

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 12, 2001, 17:12:38 ; Search time 19.52 seconds
(without alignments)
2271.188 Million cell updates/sec

Title: US-09-294-539-4

Perfect score: 2952

Sequence: 1 MEPTSHVTNAFSDSDASV.....RSLSSSSSTSGAIRPRR 582

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1276	43.2	593	F96666	hypothetical prote
2	1213.5	41.1	600	T04267	NPRI protein homol
3	985.5	33.4	601	T04747	hypothetical prote
4	441.5	15.0	467	T47773	hypothetical prote
5	421	14.3	491	H84840	hypothetical prote
6	132.5	4.5	4377	A55575	ankyrin 3, long sp
7	131.5	4.5	1016	T19006	ankyrin related pr
8	131	4.4	1856	B35049	ankyrin 1, erythro
9	131	4.4	1880	A35049	ankyrin 1, erythro
10	131	4.4	1881	1 SJHUK	ankyrin 1, erythro
11	128.5	4.4	1943	T42713	ankyrin 3, splice
12	128	4.3	1848	S37771	ankyrin, erythrocy
13	127	4.3	1765	T42714	ankyrin 3, splice
14	127	4.3	1940	T42715	ankyrin 3, splice
15	127	4.3	1961	T42716	ankyrin 3, splice
16	127	4.3	3924	S37431	ankyrin 2, neurona
17	126.5	4.3	543	C86212	hypothetical prote
18	125.5	4.3	532	G84427	hypothetical prote
19	123	4.2	1862	T49502	ankyrin - mouse
20	122.5	4.1	331	T01838	hypothetical prote
21	122	4.1	466	T33574	hypothetical prote
22	120.5	4.1	984	A41996	NF-kappa-B p50 sub
23	119.5	4.0	359	A55839	transcription fact
24	119	4.0	1963	1 MKW	myosin heavy chain
25	119	4.0	2352	T30201	Notch homolog prot
26	117.5	4.0	907	T15044	p50B/p97 (lyt-10)
27	117	4.0	211	T18174	ankyrin repeat pro
28	117	4.0	1188	2 G8396	chromosome segrega
29	116.5	3.9	323	2 B47169	ankyrin-like repea

ALIGNMENTS

RESULT 1

F96666

hypothetical protein F15H21.6 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: F96666

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon ansen, N.F.; Hughes, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: F96666

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-593 <STO>

A:Cross-references: GB:AE005173; NID:g10645392; PIDN:AAG21510.1; GSPDB:GN00141

C:Genetics:

A:Gene: F15H21.6

A:Map position: 1

Query Match 43.2%; Score 1276; DB 2; Length 593;
Best Local Similarity 47.2%; Pred. No. 3.4e-80;
Matches 273; Conservative 113; Mismatches 165; Indels 28; Gaps 9;

QY 5 TSHVTNAFSDSDASVEGDADADAVEALRLRLSDNLAAAFSPEDFAFIADARIAPVG 64

Db 17 TSFVATDNTDSSIVLAEEQVLTGPDVSALQLLSNFESVFDSPDD--FVSDAKLVL--- 71

QY 65 GGGGDLRHRCVLSARSFELRCVFAARRAAAGGGEDGSRLELLRELLGGGEEVEVG 124

Db 72 -SDGREVSFHRVLSARSFFFSALA--AAKKEKSNNTAAVKLEKEI----AKDYEVG 124

QY 125 YBALRLVLDLYLSGRVGLDPAKACLCVDECAHVGCCHPAVAFMAQVLFQAFTFQVAELTN 184

Db 125 FDSVTVLAYVYSSRVPPKGVSECADENCCVACRPAYDFMFLVLYLAFIKFELIT 184

QY 185 LFORRLDLVKVEVDNLLILSVANLCKNSCKMLERCLDMVVRNLDIMTLEKSLPPD 244

Db 185 LYQRHLLDVVDVKVIEDTLVILKLANICGACNKLDRCKEIIIVKSNVDMVSLPEE 244

QY 245 VIKQIIDARLSLGLISPEKNGFPNKHVRHRAIDSDVDVLMVRLTEGOTNLDLDAFALH 304

Db 245 LKKEIIDRRKELGLEVPKYK----KHVSNVHKALSDDDIELVKLLKEQHTNLDLDAFALH 300

QY 305 YAVEHCDSKITTELLDALADVNHNRNPRGVTYVHLHIAARRREPKEIIVSLTCKGARPADVT 364

30 116.5 3.9 439 2 J01729 ankyrin-repeat pro
31 116.5 3.9 781 2 S75367 zam protein - Syne
32 114.5 3.9 1001 2 S30385 G9a protein - huma
33 114 3.9 552 1 TWMVT3 transforming prote
34 113.5 3.8 854 2 S33558 unc-33 protein - C
35 113.5 3.8 1283 2 T29109 histidine kinase F
36 113 3.8 495 2 T27995 hypothetical prote
37 112.5 3.8 1411 2 S30355 alpha-latroinsecto
38 112.5 3.8 1786 2 A57282 ankyrin-related pr
39 112.5 3.8 1815 2 T15346 elegans ankyrin-re
40 112.5 3.8 1867 2 T15344 ankyrin-related un
41 112.5 3.8 2039 2 T15347 ankyrin-related un
42 112 3.8 397 2 T46445 hypothetical prote
43 112 3.8 880 2 F75103 conserved hypothet
44 112 3.8 1107 2 T21280 hypothetical prote
45 112 3.8 1964 2 T09059 notch4 - mouse

Db 301 FAVAYCNKVTATDLLKDLADVNHRNPRGTVLHVAAARKEPQLILSLEKGSASEATL 360
QY 365 DGRKAVOISRLTKQDYGFTVEGRPSKDRCLCIEILEQAERDQOLGASVSLAMAGE 424
Db 361 EGRALMAIAKQATMAVECCNINPEQCKHSLKGLRCVLEQEDREQIPRDVPPSFVAAD 420
QY 425 SLGRLLYLENVALARIMFPMARVAMDIAQDGTGLEFNLGSGANPPPP---ORTTV 480
Db 421 ELKMTLLDENRVALAQRLEPTEAQAAMEAKMGCEFIIVTS---LEPRLTGTRKTSR 477
QY 481 DLNESPIMKEELHARMTALSKTVELGKREFPFRCSNVLDKIMD-DETDPVSLGRDTSAAK 539
Db 478 GVKIAPPRIILEHQSLKALSKTVELGKREFPFRCSAVLDQIMNCEDLTQLACGEDDTAEK 537
QY 540 R-----KRFHLDQVLQKAFHEDKEENDRSLSSSSSTS 574
Db 538 RLOKKQRYMEIQETLKKAFSEDNLELGNSSLTDTSTSTS 576

RESULT 2
T04267
NPRI protein homolog F20B18.230 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
C:Accession: T04267
R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hohelsel, J.; Mewes, H.W.; Mayer, K.F.X.
submitted to the Protein Sequence Database, March 1999
A:Reference number: Z15263
A:Accession: T04267
A:Molecule type: DNA
A:Residues: 1-600 <BEV>
A:Cross-references: EMBL:AL049483
A:Experimental source: cultivar Columbia; BAC clone F20B18
C:Genetics:
A:Map position: 4
A:Introns: 186/3; 433/1; 501/1
A:Note: F20B18.230

Query Match 41.1%; Score 1213.5; DB 2; Length 600;
Best Local Similarity 45.8%; Pred. No. 7e-76;
Matches 277; Conservative 105; Mismatches 172; Indels 51; Gaps 17;

QY 1 MEPTSHVTAFSDSASVEEGD---ADADAD-----VEALRLSDNLAAAFR 46
Db 1 MATTTTTARFSDSYEFNTSGNSFFAESLDYPTFEULTPPVSAKLKLSLCLESVFD 60

QY 47 SPEDFAFLADARIAVPGGGGGGDLRHRCVLSARSFELRGVFAARRAAAGGGEGDGE 106
Db 61 SPE--TFYSDAKLVL---AGGREVSFRCILSARIP---VF--KSLATVKEQKSTTV 109

QY 107 RLEIRELLGGGEEVEGYEALRLVLDYLYSGRVGDLPKAACLCVDEDCAHVGCHPAVAF 166
Db 110 KLQKUEI---ARDYEGFDSVAVLAIVYSGRVSPRPGKASACVDDCCCHVACRSKVD 165

QY 167 MAQVLAFASTFQVAFNLFRLLDVLKVEVDNLLILSVANLCKSKMLLERCLDM 226
Db 166 MVEVLYLSFVQIQELVLYERQFLEIVDKVWVEDILVFELDLCTGTYTKLLDRDCEI 225

QY 227 VVRNLDMLTEKSLPPDVIKQIIDAKLSGLISPENKGFNKHVRHIALSDDDVELV 286
Db 226 IVKSDIELVSLKSLPQHIFKQIIDREALCLEPPKLE---RHVKNYKALSDDDVELV 281

QY 287 RMLLTEGOTLDDAFALHYAVEHCDSKITTELADLVNHRNPRGTVLHIAARREP 346
Db 282 KMLLEGTNLDDEAYALHFAHCAVATAYDILLELEADVNLNRPRTVYLHVAAARKEP 341

QY 347 KIIIVSLTKGARPADVTDFGRKAVQISKRLLTKQDYGFTVEGRPSKDRCLCIEILBQAE 406
Db 342 KLIISLLMKGANILDTLDRGTALVIVKRLTKADDTSTEDGTPSLKGGCLIEVLEH-E 400

QY 407 RRDQPLG--EASVSLAMAGESLRRLYLENVALARIMFPMARVAMDIAQDGTGLEFN 464

Db 401 QKLEYLSPEASLSLPTPEELRMRLLYENRVALARLLFPVETVQGIKLEETCEFT 460
QY 465 LGSANPPPE--RQRTVDLINESPFFIMKEELHARMTALSKTVELGKREFPFRCSNVLDKIM 522
Db 461 -ASSLEPDDHHIGBKRTSLDNLMAFPQIHEKHLRLKALCKTVELGKRYFKRCS--LDHEM 517
QY 523 DDE--TDPVSLGRDT---SAEKKRPFHDLDQVLQKAFHEDKEENDRSLSSSSSTSIGA 577
Db 518 DTEDLNLHLSAVEDETPPEKRLQKQRYMELQETLMKTFESEDKEE---CGKSSSTPKPTS--A 572

QY 578 IRPRR 582
Db 573 VRGSR 577

RESULT 3
T04747
hypothetical protein T16H5.20 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
C:Accession: T04747
R:Bevan, M.; De Haan, M.; Maarse, A.C.; Grivell, L.A.; Bancroft, I.; Mewes, H.W.; May
submitted to the Protein Sequence Database, June 1998
A:Reference number: Z15383
A:Accession: T04747
A:Molecule type: DNA
A:Residues: 1-601 <BEV>
A:Cross-references: EMBL:AL024486
A:Experimental source: cultivar Columbia; BAC clone T16H5
C:Genetics:
A:Map position: 4
A:Introns: 173/3; 420/1
A:Note: T16H5.20

Query Match 33.4%; Score 985.5; DB 2; Length 601;
Best Local Similarity 40.8%; Pred. No. 3.5e-60;
Matches 242; Conservative 96; Mismatches 170; Indels 85; Gaps 18;

QY 34 LRLRLSDNLAAAFRSPEDFAFLADARIAVPGGGGGGDLRHRCVLSARSFELRGVFAARR 92
Db 35 LEELSSNLEQLLTNPDCDY---TDAELIIE---EENPVSVHRCVLAARSKFFLDLFFK- 87

QY 93 AAAAAAGGGEGDGE---RLEIRELLGGGEEVEGYEALRLVLDYLYSGRVGDLPKAACL 149
Db 88 -----DKDSSEKKPKYQMKDLLPYG---NVGREAFHLFLSYIVTGRLLKPPPIEVST 135

QY 150 CVDEDCAHVGCHPAVAFMAQVLAFAASTFQVAFNLFRLLDVLKVEVDNLLILSVA 209
Db 136 CVDSVCAHDSCKPAIDPAVELMYASFVQIPDLVSSFORKLRNVKESLVENLPIILVA 195

QY 210 NLCKSKMLLEKCLDMVVRNLDMLTEKSLPPDVIKQIIDARL-SLGLISPENKGFN 268
Db 196 FHCDLT---QLDQCIEIARVARSDDRFCEIKELPLEVLEKIKQLRVKSVNPIVEDEKSI-- 251

QY 269 KHVRIIRALSDSDVELVRMLLTGEGQTNLDDAFALHYAVEHCDSKITTELADLVN 328
Db 252 ERTGKVLKALSDSDVELVKKLLTESDITLDQANGLHVAVAYSDPKVVTQVLDLMDADVNE 311

QY 329 RNPFGYTVLHIAARRRPKIIVSLLTGAPADVTDFGRKAVQISKRLLTKQDYGFTVEE 388
Db 312 RNSRGYTVLHIAARRRPKIIVSLLTGAPADVTDFGRKAVQISKRLLTKQDYGFTVEE 371

QY 389 GKSPKDRCLCIEILEQAERDQOLGASVSLAMAGESLRRLYLENVALARIMFPM 447
Db 372 KEPS-KYRLCIDILEREIRNPLVSGDTPCCHSNMPEDLQMLRLYLEKRVGLAQLPFAE 430

QY 448 ARVAMDAQVDGDTGLEFNLGSGANPPPPRQRT-----VDLNESPFIMKEELHARMTALSK 502
Db 431 ANVAMDVANVESTSEC---TGLLTPPPSNDTLENLGVLDNETPYVQTKRMLTKRMALMK 487

QY 503 T-----VELGKREFPFRCSNVLDKIMD---DETDPVSLG 532

Db 488 TCKSLRCKTFKFSYLTTLTLDTSKPFNNVETGRRYFPSCYEVLDKYMQDMEIP---- 543
 QY 533 RDTSS-----AKKRRFHDLDVLOKAFHEKDEKNDKSLSSSSSTSI 575
 Db 544 -DMSYPEKGTVKERRQKRMRYNELNDVKYKSKVA--RSLSSSPASSL 593

RESULT 4

T47773

hypothetical protein F2413.210 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C:Accession: T47773

R:Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;

submitted to the Protein Sequence Database, February 2000

A:Reference number: 224475

A:Accession: T47773

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-467 <NYA>

A:Cross-references: EMBL:AL138655

A:Experimental source: cultivar Columbia; BAC clone F2413

C:Genetics:

A:Map position: 3

A:Introns: 157/3

A:Note: F2413.210

Query Match 15.0%; Score 441.5; DB 2; Length 467;
 Best Local Similarity 30.8%; Pred. No. 7.2e-23;
 Matches 137; Conservative 72; Mismatches 169; Indels 67; Gaps 16;

QY 32 EALRRLS---DNLAFAFRSPEDFAFLADARIAVPGGGGGDLRVHRCVLSARSFPLRGV 88
 Db 7 ELSKNSLDYLNLLINGQAFSDVTSVEGRL-----VHAHRCILAARSLEFRKF 55
 QY 89 FARRAAAAAGG--GGDGERLELRLGGGEEV--EVGEALRLVDLYSGRGVDLP- 144
 Db 56 FCESDPSQGAEPANGTGS---GARAAGVGVPVNSGYEVFELLQLLYSGQSVIVPH 112
 QY 145 --KAACLCVDECAHVCHPVAFAQVLFPAASTFOVAELTNLFORRLDVKVEVDNL 202
 Db 113 KHEPRNCNCDRGCHWTHCTAAVDLSLDILAAARFVCGEQLALLTQKHLTSMVEKASIEDV 172
 QY 203 LLILSVANLCNCKMCKLLERCLDMVVRSLDMLTLEKSLPPDVVKOIIDARLSGLISPE 262
 Db 173 MKVLIASR--KQDMHQLWTTCSTLYIAKSGLPQEIILAKHLPIELVAKIEELRLKSSM--PL 228
 QY 263 NKGFPPNKH-----VRRIRHALSDSDVELVRLMTEGQTNLDLDAFALHYAVEHC 310
 Db 229 RSLMPHHHDLTSTLDLEDQKIRMRRLDSSDVELVKLMVMEGLNDESALIYAVENC 288
 QY 311 DSKITTELLDLADLVNH--RNPRGYTVLHIAARRRPEKIIIVSLITKGARPADVTFDGRKA 369
 Db 289 SREVVKALLEGAADVNYVPAGPTGKTALHIAAEMVSPDMVAVLLDDHADPNVQTVGDIPT 348
 QY 370 VQISKRLTK-----QGDYFGVTEGKSPKDRICIELEQA-----ERRD----- 409
 Db 349 LDILRLTSDFLFKGAIPGLTHI-EPN-KLRCLCLEVQSAALVISREEGNNNSNDNNTMI 406
 QY 410 -POLGEASVSLAMAGSLRGLLYL 433
 Db 407 YPMKDEHTS-----GSSLDRLVYL 427

RESULT 5

H84840

hypothetical protein At2g41370 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: H84840

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487
 A:Accession: H84840
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-491 <STO>
 A:Cross-references: GB:AE002093; NID:g3894187; PIDN:AAC78536.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g41370
 A:Map position: 2

Query Match 14.3%; Score 421; DB 2; Length 491;
 Best Local Similarity 29.2%; Pred. No. 2e-21;
 Matches 135; Conservative 72; Mismatches 170; Indels 86; Gaps 15;

QY 32 EALRRLS---DNLAFAFRSPEDFAFLADARIAVPGGGGGDLRVHRCVLSARSFPLRGV 88
 Db 6 ELSRLSLDLFLNLLINGQAFSDVTSVEGRL-----VHAHRCILAARSLEFRKF 54
 QY 89 FARRAAAAAGGCGDGERLELRLGGGEEV-----EVGEALRLV 132
 Db 55 FC-----GTDSPQPVGTGIDPTQHGVSVPASPTRGSTAPAGIIPVNSGVYEVFLLLL 104
 QY 133 DYLSGRVGDLP---KAACLCVDECAHVCHPVAFAQVLFPAASTFOVAELTNLFQRR 189
 Db 105 QFLYSGQSVIVPQKHEPRNCGERGCHWTHCTAAVDLALDITLAASRYFVGEQALLTQK 164
 QY 190 LLDVLDKVEVDNLLILSVANLCNCKMCKLLERCLDMVVRSLDMLTLEKSLPPDVVKOII 249
 Db 165 LASWEKASIEDVMKVLIASR--KQDMHQLWTTCSTLYIAKSGLPPEILAKHLPIDVVTKI 222
 QY 250 IDARLSGL-----ISPEN-----KGFPNKHVRRIRHALSDSDVELVRLMTEGQTNL 297
 Db 223 EELRLKSSITARRSLMPHHHDLSDVAQDLEDQKIRMRRLDSSDVELVKLMVMEGLNL 282
 QY 298 DDAFALHYAVEHCDSKITTELLDLADLVNH--RNPRGYTVLHIAARRRPEKIIIVSLITKG 356
 Db 283 DESLALHYAVESCSEVVKALLEGAADVNYVPAGPTGKTALHIAAEMVSPDMVAVLLDDH 342
 QY 357 ARPADVTFGKRAVQISKRLTK---QGDYFGVTEGKSPKDRICIELEQA----- 405
 Db 343 ADPNVTGCGITPLDILRLTSDFLFKGAIPGLTHI-EPN-KLRCLCLEVQSAALVISRE 400
 QY 406 -----ERRD-----POLGEASVSLAMAG--ESLGRGLLYL 433
 Db 401 EGNNSNNQNDNNTGIYPHMEHNSGSGGNNNLDRLVYL 443

RESULT 6

A55575

ankyrin 3, long splice form - human

N:Alternate names: ankyrin G

C:Species: Homo sapiens (man)

C>Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 20-Sep-1999

C:Accession: A55575

R:Kordeli, E.; Lambert, S.; Bennett, V.

J. Biol. Chem. 270, 2352-2359, 1995

A:Title: Ankyrin-G. A new ankyrin gene with neural-specific isoforms localized at the

A:Reference number: A55575; MUID:95138209

A:Accession: A55575

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-4377 <KOR>

A:Cross-references: GB:U13616; NID:g608024; PIDN:AAA64834.1; PID:g608025

C:Genetics:

A:Gene: GDB:ANK3

A:Cross-references: GDB:424503; OMIM:600465

A:Map position: 10q21-10q21

C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol

C: Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998
 R: Accession: B35049
 R: Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.;
 Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
 A: Title: cDNA sequence for human erythrocyte ankyrin.
 A: Reference number: A35049; MUID: 90175370

C: Accession: B35049
 A: Status: preliminary
 A: Molecule type: mRNA
 A: Residues: 1-1856 <LAM>
 C: Genetics:
 A: Gene: GDB: ANK1; ANK
 A: Cross-references: GDB: 118737; OMIM: 182900
 A: Map position: 8p11.2-8p11.2
 C: Superfamily: ankyrin; ankyrin repeat homology
 C: Keywords: alternative splicing
 F: 2-1856/Product: ankyrin 1, erythrocyte form 3 #status predicted <MAT>
 F: 2-1513/1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>
 F: 44-76/Domain: ankyrin repeat homology <AN01>
 F: 77-109/Domain: ankyrin repeat homology <AN02>
 F: 110-142/Domain: ankyrin repeat homology <AN03>
 F: 143-171/Domain: ankyrin repeat homology <AN04>
 F: 172-204/Domain: ankyrin repeat homology <AN05>
 F: 205-237/Domain: ankyrin repeat homology <AN06>
 F: 238-270/Domain: ankyrin repeat homology <AN07>
 F: 271-303/Domain: ankyrin repeat homology <AN08>
 F: 304-336/Domain: ankyrin repeat homology <AN09>
 F: 337-369/Domain: ankyrin repeat homology <AN10>
 F: 370-402/Domain: ankyrin repeat homology <AN11>
 F: 403-435/Domain: ankyrin repeat homology <AN12>
 F: 436-468/Domain: ankyrin repeat homology <AN13>
 F: 469-501/Domain: ankyrin repeat homology <AN14>
 F: 502-534/Domain: ankyrin repeat homology <AN15>
 F: 535-567/Domain: ankyrin repeat homology <AN16>
 F: 568-600/Domain: ankyrin repeat homology <AN17>
 F: 601-633/Domain: ankyrin repeat homology <AN18>
 F: 634-666/Domain: ankyrin repeat homology <AN19>
 F: 667-699/Domain: ankyrin repeat homology <AN20>
 F: 700-732/Domain: ankyrin repeat homology <AN21>
 F: 733-765/Domain: ankyrin repeat homology <AN22>
 F: 766-798/Domain: ankyrin repeat homology <AN23>

Query Match 4.4%; Score 131; DB 2; Length 1856;
 Best Local Similarity 23.6%; Pred. No. 1-2;
 Matches 75; Conservative 34; Mismatches 103; Indels 106; Gaps 12;

QY 271 VRRHRLDSDDELVELVRLMT-----EGQTNLDLDAF----- 301
 DB 636 VTPHLAAQEGHAEMVALLSKQANGNLGNKSGLTPLHLVAQEGHVPADVLIKHGVMVD 695
 QY 302 -----ALHYAVEHCDSKITTELLDALADYNHNRPRGYTVLHIAARREPKIIVSLL 353
 DB 696 ATTRMGVTPHLVAHSHYGNIKLVKFLQ-HQADYNNAKTGLGYSPLHQAQOQGHDTIVTLL 754
 QY 354 TKGARPADVTFDGRKAVQISKRLLTKQDYGFGVTEEG-----PSPKDRLCI----- 399
 DB 755 KNGASPNVSSDGTTPLAIAKRL-----GYISVTDVLKVVTDTSFVLVSKHRMSFPETV 810
 QY 400 -EILEQARERDPOLGEASVSLAMAGESLRGLLYLENVALARIMFPMPEARVAMDIQVND 458
 DB 811 DEILDVSEDE-----GEEL-----ISFKAERDRSDVDEEK 841
 QY 459 GTLEFNLGSGANPPPERQRTTVDLNEPSFTMKKEHLARMTALSKTVELGKRFPPRCNVL 518
 DB 842 ELLDF-----VPKLDQVV-----ESPAIPRI-----CAMPETVVIRSEEQASKEY 884
 QY 519 DKTMDDTDPVSLGRDTS 536
 DB 885 D-----EDSLIPSPATETS 899

RESULT 9

A35049
 ankyrin 1, erythrocyte splice form 2 - human
 N: Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
 N: Contains: ankyrin 2.2, erythrocyte
 C: Species: Homo sapiens (man)
 C: Date: 27-Jul-1990 #sequence_revision 01-Oct-1992 #text_change 04-Sep-1998
 R: Accession: A35049
 R: Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.;
 Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
 A: Title: cDNA sequence for human erythrocyte ankyrin.
 A: Reference number: A35049; MUID: 90175370

C: Accession: A35049
 A: Status: preliminary
 A: Molecule type: mRNA
 A: Residues: 1-1880 <LAM>
 A: Cross-references: GB: M28880
 C: Genetics:
 A: Gene: GDB: ANK1; ANK
 A: Cross-references: GDB: 118737; OMIM: 182900
 A: Map position: 8p11.2-8p11.2
 C: Superfamily: ankyrin; ankyrin repeat homology
 C: Keywords: alternative splicing; cytoskeleton
 F: 2-1880/Product: ankyrin 1, erythrocyte form 2 #status predicted <MAT>
 F: 2-1513/1676-1880/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>
 F: 44-76/Domain: ankyrin repeat homology <AN01>
 F: 77-109/Domain: ankyrin repeat homology <AN02>
 F: 110-142/Domain: ankyrin repeat homology <AN03>
 F: 143-171/Domain: ankyrin repeat homology <AN04>
 F: 172-204/Domain: ankyrin repeat homology <AN05>
 F: 205-237/Domain: ankyrin repeat homology <AN06>
 F: 238-270/Domain: ankyrin repeat homology <AN07>
 F: 271-303/Domain: ankyrin repeat homology <AN08>
 F: 304-336/Domain: ankyrin repeat homology <AN09>
 F: 337-369/Domain: ankyrin repeat homology <AN10>
 F: 370-402/Domain: ankyrin repeat homology <AN11>
 F: 403-435/Domain: ankyrin repeat homology <AN12>
 F: 436-468/Domain: ankyrin repeat homology <AN13>
 F: 469-501/Domain: ankyrin repeat homology <AN14>
 F: 502-534/Domain: ankyrin repeat homology <AN15>
 F: 535-567/Domain: ankyrin repeat homology <AN16>
 F: 568-600/Domain: ankyrin repeat homology <AN17>
 F: 601-633/Domain: ankyrin repeat homology <AN18>
 F: 634-666/Domain: ankyrin repeat homology <AN19>
 F: 667-699/Domain: ankyrin repeat homology <AN20>
 F: 700-732/Domain: ankyrin repeat homology <AN21>
 F: 733-765/Domain: ankyrin repeat homology <AN22>
 F: 766-798/Domain: ankyrin repeat homology <AN23>

Query Match 4.4%; Score 131; DB 2; Length 1880;
 Best Local Similarity 23.6%; Pred. No. 1-2;
 Matches 75; Conservative 34; Mismatches 103; Indels 106; Gaps 12;

QY 271 VRRHRLDSDDELVELVRLMT-----EGQTNLDLDAF----- 301
 DB 636 VTPHLAAQEGHAEMVALLSKQANGNLGNKSGLTPLHLVAQEGHVPADVLIKHGVMVD 695
 QY 302 -----ALHYAVEHCDSKITTELLDALADYNHNRPRGYTVLHIAARREPKIIVSLL 353
 DB 696 ATTRMGVTPHLVAHSHYGNIKLVKFLQ-HQADYNNAKTGLGYSPLHQAQOQGHDTIVTLL 754
 QY 354 TKGARPADVTFDGRKAVQISKRLLTKQDYGFGVTEEG-----PSPKDRLCI----- 399
 DB 755 KNGASPNVSSDGTTPLAIAKRL-----GYISVTDVLKVVTDTSFVLVSKHRMSFPETV 810
 QY 400 -EILEQARERDPOLGEASVSLAMAGESLRGLLYLENVALARIMFPMPEARVAMDIQVND 458
 DB 811 DEILDVSEDE-----GEEL-----ISFKAERDRSDVDEEK 841
 QY 459 GTLEFNLGSGANPPPERQRTTVDLNEPSFTMKKEHLARMTALSKTVELGKRFPPRCNVL 518
 DB 842 ELLDF-----VPKLDQVV-----ESPAIPRI-----CAMPETVVIRSEEQASKEY 884

QY 368 KAVQISKRL----- 376
 Db 781 TALAIARLGYISVVDLTKVTEIMTTTITEKHKMNPETNEVLNDSDEVRKASAP 840
 QY 377 --TKQGDYFGVTEEGKPS-----PKDRLCIEILEQAERRDPOLGEASVSLAMAGE 424
 Db 841 EKLSDGEYISDGEEDAIKGTGDKVLGPQD-----LKELGDDSLPAEGYVGFSLGARS 895
 QY 425 SLR---GRLLYLENVALAR 441
 Db 896 SLRFSFSDRSYTLNRSSYAR 915
 RESULT 12
 S37771
 ankyrin, erythrocyte - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 27-May-1994 #sequence_revision 03-Aug-1995 #text_change 13-Aug-1999
 C:Accession: S37771
 R:Birkenmeier, C.S.; White, R.A.; Peters, L.L.; Hall, E.J.; Lux, S.E.; Barker, J.E.
 J. Biol. Chem. 268, 9533-9540, 1993
 A:Title: Complex patterns of sequence variation and multiple 5' and 3' ends are found am
 A:Reference number: S37771; MUID:93252825
 A:Accession: S37771
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1848

 A:Cross-references: EMBL:X69063; NID:g311816; PIDN:CAA48801.1; PID:g311817
 C:Superfamily: ankyrin; ankyrin repeat homology
 C:Keywords: alternative splicing
 F:81-113/Domain: ankyrin repeat homology <AN01>
 F:114-146/Domain: ankyrin repeat homology <AN02>
 F:147-175/Domain: ankyrin repeat homology <AN03>
 F:176-208/Domain: ankyrin repeat homology <AN04>
 F:209-241/Domain: ankyrin repeat homology <AN05>
 F:242-274/Domain: ankyrin repeat homology <AN06>
 F:275-307/Domain: ankyrin repeat homology <AN07>
 F:308-340/Domain: ankyrin repeat homology <AN08>
 F:341-373/Domain: ankyrin repeat homology <AN09>
 F:374-406/Domain: ankyrin repeat homology <AN10>
 F:407-439/Domain: ankyrin repeat homology <AN11>
 F:440-472/Domain: ankyrin repeat homology <AN12>
 F:473-505/Domain: ankyrin repeat homology <AN13>
 F:506-538/Domain: ankyrin repeat homology <AN14>
 F:539-571/Domain: ankyrin repeat homology <AN15>
 F:572-604/Domain: ankyrin repeat homology <AN16>
 F:605-637/Domain: ankyrin repeat homology <AN17>
 F:638-670/Domain: ankyrin repeat homology <AN18>
 F:671-703/Domain: ankyrin repeat homology <AN19>
 F:704-736/Domain: ankyrin repeat homology <AN20>
 F:737-769/Domain: ankyrin repeat homology <AN21>
 F:770-802/Domain: ankyrin repeat homology <AN22>
 Query Match 4.3%; Score 128; DB 2; Length 1848;
 Best Local Similarity 23.7%; Pred. No. 1.9;
 Matches 58; Conservative 31; Mismatches 78; Indels 78; Gaps 8;
 QY 271 VRRTHRALSDVRLVRLMLT-----EGQTNLDDAF----- 301
 Db 640 VTPLHLAAQEGHTEKXVALLSKQANGLNKSGLTPLHLVYSEGHVPVADVLIKHGVTVD 699
 QY 302 -----ALHYAVEHCDSKITTELLDALADVNRHNRPGYTVLHIAARRRPREKIIVSL 353
 Db 700 ATTRMGYTPHLVASHYGNIKLVKFLQ--HQADVNAKTKLGYSPHLQAQOQGHDTIVTLL 758
 QY 354 TKGARPADVTDFGRKAVQISKRLTKQDYGVTVEGK-----PSPKDLICI----- 399
 Db 759 KNGASPNVSSNGTPTLAIAKRL-----GYISVTDVLKVVTDTSVVLVSKHRMSYPET 814
 QY 400 -EILEQAERRDPOLGEASVSLAMAGESLGRLLYLENVALARIMFPWEARVAMDAQVD 458

Db 815 DEILDVSE-----DEGTAHISIMGDELVS-----KAERRSDRVGEER 853
 QY 459 GTLEF 463
 Db 854 ELLDF 858
 RESULT 13
 T42714
 ankyrin 3, splice form 2 - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
 C:Accession: T42714
 R:Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo
 J. Cell Biol. 130, 313-330, 1995
 A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin ge
 the repeat domain.
 A:Reference number: 222237; MUID:95340633
 A:Accession: T42714
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1765 <PET>
 A:Cross-references: EMBL:L40632; NID:g710548; PID:g710551; PIDN:AAB01605.1
 A:Experimental source: strain C57BL/6J; kidney
 C:Genetics:
 A:Gene: Ank3
 A:Map position: 10
 A:Introns: 1587/1
 C:Superfamily: ankyrin; ankyrin repeat homology
 C:Keywords: alternative splicing
 Query Match 4.3%; Score 127; DB 2; Length 1765;
 Best Local Similarity 32.6%; Pred. No. 2;
 Matches 42; Conservative 20; Mismatches 59; Indels 8; Gaps 4;
 QY 254 LSLGLISPENKGFNKH-VRRHRLSDSDVRLVRLMLTTEG-----QTNLDDAFALHYAV 307
 Db 663 VSLLSRNANVNLNKSGLTPLHLAQEDRVNVAEVLVNOGAHVDAQTKMGYT-PLHVG 721
 QY 308 EHCDSKITTELLDALADVNRHNRPGYTVLHIAARRRPREKIIVSLLPKGARPADVTDFGR 367
 Db 722 HYGNIKIVNELLQHS-AKVNAKTKNGYATLHQAQOQGHITHIINVLQNNASPNELTVNGN 780
 QY 368 KAVQISKRL 376
 Db 781 TALAIARRL 789
 RESULT 14
 T42715
 ankyrin 3, splice form 3 - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
 C:Accession: T42715
 R:Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo
 J. Cell Biol. 130, 313-330, 1995
 A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin ge
 the repeat domain.
 A:Reference number: 222237; MUID:95340633
 A:Accession: T42715
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1940 <PET>
 A:Cross-references: EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01604.1
 A:Experimental source: strain C57BL/6J; kidney
 C:Genetics:
 A:Gene: Ank3
 A:Map position: 10
 A:Introns: 834/1
 C:Superfamily: ankyrin; ankyrin repeat homology
 C:Keywords: alternative splicing

Query Match	4.3%;	Score 127;	DB 2;	Length 1940;
Best Local Similarity	32.6%;	Pred. No. 2.3;		
Matches	42;	Conservative 20;	Mismatches 59;	Indels 8; Gaps 4;
QY	254	LSLGLISPENKGFPNKH-VRIHRIALDSDVDVLYRMLLTEG-----QTNLDDAFALHYAV	307	
		: : : : : : : : : :		
Db	663	VSLLSLRNANVLNSKGLTFLHLAAQEDRVNVAEVLNQGAHVDAQTKMGYT-PLHVGC	721	
QY	308	EHCDSKTITTELDLIALADVNHRNPRTVTLVHIAARRREPKIIVSILTKGARPDADVTFDGR	367	
		: : : : : : : : : :		
Db	722	HYGNIKIVNFLQHS-AKVNAKTNGTYALTALHQAAQQGHTHIINVLQNNASPNELTVNGN	780	
QY	368	KAVOISRKL	376	
		: : : : : : : : : :		
Db	781	TALAIAIARRL	789	

RESULT 15

RESULT 15
T42716
ankyrin 3, splice form 4 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jan-2000 #sequence_revision 1
C:Accession: T42716
R:Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Vialamas, M.; Turtzo, I.
J. Cell Biol. 130, 313-330, 1995
A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
the repeat domain.
A:Reference number: 222237; MUID:95340633
A:Accession: T42716
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1961 <P>
A:A:Cross-references: EMBL:L40632; NID:g710548; PID:g710552; PIDN:AAB01607.1
A:Experimental source: strain C57BL/6J; kidney
C:Genetics:
A:Gene: Ank3
A:Map position: 10
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing

	Query Match	4.3%	Score 127;	DB 2;	Length 1961;
	Best Local Similarity	32.6%	Pred. No. 2.4;		
	Matches	42;	Conservative	20;	Mismatches 59; Indels 8; Gaps 4;
QY	254	LSLGLISPENKGP	PNKH-VRRIRH	ALSDSDV	ELVRLMLTTEG-----QTNLDDAFALHYAV 307
		:::::	:::::	:::::	:::::
Db	663	VSLLSSNANVLS	NSGLTPLHLAAQ	EDRVNVAE	LVNQAQAHVDAQTKMYT-PLHVGC 721
		:::::	:::::	:::::	:::::
QY	308	EHCDSKTITTE	LLOLADLVNHR	PNRGVTVL	HIARREPKIIIVSLTKGARPADVTFDGR 367
		:::::	:::::	:::::	:::::
Db	722	HYGNIKIVNELL	QHS-AKVNAK	YKNGYTA	LHQAAQOQGHTHIINVLLQNNASPNELTVNGN 780
		:::::	:::::	:::::	:::::
QY	368	KAVOISKRL	376		
		:::::	:::::		
Db	781	TALAIARRL	789		
		:::::	:::::		

Search completed: July 12, 2001, 17:14:01
Job time: 83 sec

[illegible]

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Qy 61 VPGGGGGGLRVHRCVLSARSPLRGVFAARRAAAAAGGGGGEDSERLELRELLGGGEE 120
Db 61 VPGGGGGGLRVHRCVLSARSPLRGVFAARRAAAAAGGGGGEDSERLELRELLGGGEE 120
Qy 121 VEVGYEARLRLVDLYISGRVGDLPKAAACLCVDECAHVGCHPAVAFMAQVLFPAASTFQVA 180
Db 121 VEVGYEARLRLVDLYISGRVGDLPKAAACLCVDECAHVGCHPAVAFMAQVLFPAASTFQVA 180
Qy 181 ELTNLFQRLLDVLDKVEVDNLLILSVANLCNCKSMKLLERCLDMVVRNLDMLITLEKS 240
Db 181 ELTNLFQRLLDVLDKVEVDNLLILSVANLCNCKSMKLLERCLDMVVRNLDMLITLEKS 240
Qy 241 LPPDVIKOIIDARLSGLISPENKGFNKHVRRIHRAALSDDDVELVRLMLTTEGQTNLDDA 300
Db 241 LPPDVIKOIIDARLSGLISPENKGFNKHVRRIHRAALSDDDVELVRLMLTTEGQTNLDDA 300
Qy 301 FALHYAVEHCDKSKITTELLDALADVNHRNPRGYTVLHIAARRREPKIIVSLLTGKARPA 360
Db 301 FALHYAVEHCDKSKITTELLDALADVNHRNPRGYTVLHIAARRREPKIIVSLLTGKARPA 360
Qy 361 DVTEDGRKAVOISKRLTKQGDYFGVTEEGKSPKDRLCIEILEQAERDPOLGEASVSLA 420
Db 361 DVTEDGRKAVOISKRLTKQGDYFGVTEEGKSPKDRLCIEILEQAERDPOLGEASVSLA 420
Qy 421 MAGESLRGLLYLENRVALARIMFPMPEARVAMDIQVDTGLEFNLGSGANPPPQRQRTTV 480
Db 421 MAGESLRGLLYLENRVALARIMFPMPEARVAMDIQVDTGLEFNLGSGANPPPQRQRTTV 480
Qy 481 DLNESPFIMKEEHLARMTALSKTVELGKRFPFRCNSVLDKIMDDTDPVSLGRDTSABKR 540
Db 481 DLNESPFIMKEEHLARMTALSKTVELGKRFPFRCNSVLDKIMDDTDPVSLGRDTSABKR 540
Qy 541 KRFHDLQVLDQKAFHEDKEENDRSGLSGSSSSSTSGTGAIRPRR 582
Db 541 KRFHDLQVLDQKAFHEDKEENDRSGLSGSSSSSTSGTGAIRPRR 582
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P93002 PRELIMINARY; PRT; 593 AA.
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AC P93002; 004742;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE REGULATORY PROTEIN NPRI.
GN NPRI OR NIM1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ECOTYPE COLUMBIA;
RX MEDLINE=97148688; PubMed=9019406;
RA Cao H., Glazebrook J., Clarke J.D., Volko S., Dong X.;
RT "The Arabidopsis NPRI gene that controls systemic acquired resistance
encodes a novel protein containing ankyrin repeats.";
RL Cell 88:57-63(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Ryals J., Weymann K., Lawton K., Friedrich L., Ellis D., Steiner H.Y.,
RA Johnson J., Delaney T.P., Jesse T., Vos P., Uknes S.;
RL Plant Cell 9:0-0(0).
DR EMBL; U76707; AAC49611.1; -
DR EMBL; U87794; AAB58262.1; -
DR Mendel; 12931; Arath;2131;12931.
DR InterPro; IPR00210; -
DR Pfam; PF00023; ank; 2.
DR Pfam; PF00651; BTB; 1.
DR PROSITE; PS50086; ANK_REPEAT; 1.
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DR PROSITE; PS50297; ANK_REPEAT; 1.
DR PROSITE; PS50097; BTB; 1.
SQ SEQUENCE 593 AA; 66031 MW; DDD618146254CD68 CRC64;

Query Match 43.2%; Score 1276; DB 10; Length 593;
Best Local Similarity 47.2%; Pred. No. 3.2e-80;
Matches 273; Conservative 113; Mismatches 165; Indels 28; Gaps 9;

Qy 5 TSHVTNFAFSDSDSASVEGADADADVEALRRLLSDNLAARSPEDFAFLADARIAPGG 64
Db 17 TSFVATNTDSSIVYLAEEQVLTGPDYSALQLLSNFSFVDSPPD--FYSDAKLVL--- 71
Qy 65 GGGGGLRVHRCVLSARSPLRGVFAARRAAAAAGGGGGEDSERLELRELLGGGEEVGG 124
Db 72 -SDGREVSFHCVLARSASSFFKSALA--AAKKEKDSNTAAVKLEKEI-----AKDVEG 124
Qy 125 YEALRLVDLYISGRVGDLPKAAACLCVDECAHVGCHPAVAFMAQVLFPAASTFQVAELTN 184
Db 125 FDSVTVTLAYVYSSKVRPPPKGVSECADENCHVACRPVDFMELVLYLAFIKIPELIT 184
Qy 185 LFQRLLDVLDKVEVDNLLILSVANLCNCKSMKLLERCLDMVVRNLDMLITLEKSLLPPD 244
Db 185 LYQRHLLDVVDKVIETDVLILKLANICGKACMKLLDRCKEIIIVKSNVDMVSLKSLPEE 244
Qy 245 VIKOIIDARLSGLISPENKGFNKHVRRIHRAALSDDDVELVRLMLTTEGQTNLDDAFALH 304
Db 245 LVKEIIDRRKELGLEVPKVK---KHVSNVHKAALSDDDIELVKLLKREDHNLDDACALH 300
Qy 305 YAVEHCDKSKITTELLDALADVNHRNPRGYTVLHIAARRREPKIIVSLLTGKARPAVDTF 364
Db 301 FAVACNVKATATDLKLADVNHRNPRGYTVLHVAAMRKEPQILSLLEKGSASEATL 360
Qy 365 DGRKAVOISKRLTKQGDYFGVTEEGKSPKDRLCIEILEQAERDPOLGEASVSLAMAGE 424
Db 361 EGRALMIKATQWAVECNPIEQCKHSLKGLRCLVEILEQEDKKEQIPROVPPSFVAAD 420
Qy 425 SLRGLLYLENRVALARIMFPMPEARVAMDIQVDTGLEFNLGSGANPPP---ORRTV 480
Db 421 ELKMTLLDENRVALAQRLFPTEAQAAMEIAEMKGTCEFIIVTS---LEPDLRTGKRTSP 477
Qy 481 DLNESPFIMKEEHLARMTALSKTVELGKRFPFRCNSVLDKIMDDTDPVSLGRDTSABKR 539
Db 478 GVKIAPFRILEHOSRLKALSKTVELGKRFPFRCNSVLDQIMNCEDLTLQACGEDDTAEK 537
Qy 540 R---KRFHDLQVLDQKAFHEDKEENDRSGLSGSSSSSTSS 574
Db 538 RLQKQRYMEIQETLTKAFSEDNLELGNSSLTDTSSSTS 576

RESULT 3
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ID Q9SZI3;
AC Q9SZI3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE NPRI LIKE PROTEIN.
GN F20B18.230 OR AT4G26120.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Rose M., Hempel S., Entian K.-D., Hoheisel J., Mewes H.W.,
RA Mayer K.F.X., Schueller C.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsids sequencing project;
RA Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
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RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL049483; CAB39677.1; -;
DR EMBL; AL161564; CAB79467.1; -;
DR InterPro; IPR000210; -;
DR Pfam; PF00023; ank; 2;
DR Prosite; PS50088; ANK_REPEAT; 1;
DR Prosite; PS50297; ANK_REPEAT; 1;
DR SMART; SM00248; ANK; 1;
SQ SEQUENCE 600 AA; 68006 MW; E32D3A1ED62ACB74 CRC64;

Query Match 41.1%; Score 1213.5; DB 10; Length 600;
Best Local Similarity 45.8%; Pred. No. 6.9e-76;
Matches 277; Conservative 105; Mismatches 172; Indels 51; Gaps 17;

QY 1 MPPYTHVNTAFSDSDSASVEEGD-----ADADAD-----VEALRRLLSDNLAAR 46
DB 1 MATTTTITTTARSDSEVFNSTSGNFFAAESSLDYPTFTPEVSALKLLSNCLESVD 60
QY 47 SPEDFAFLADARAVPGGGGGDLRVHRCVLSARSFPLRGVFAARRAAAGGGGEGDSE 106
DB 61 SPE--TFYSDAKLVL-----AGGREVSFHRCLISARIP-----VF-KSALATVREKRSSTTV 109
QY 107 RLELRELLGGGEEVGVYEALRLDLXLSGRVGDLPKAAACLCVDEDAHVCHCPAVAF 166
DB 110 KQLQKEI-----ARDYEVGDSVVAVLAVYSGVRSPPKGASACVDDCCHVACKSKVDF 165
QY 167 MAQVFAAFTQVAELTNFQRRLDLVDKVEVDNLLILSVANLCNCKMKLLERCLDM 226
DB 166 MVEVLVSFVQIQELVLYERQFLVDKVVVEDILVIFKLDITCGTYKKLLDRCI 225
QY 227 VVRSNDMTLEKSLPPDVIKQIIDARLGLISPEKNGFPNKHVRIHRLDSDDEVLV 286
DB 226 IVKSDIELVLSKSLPQHIFKQIIDREALCLEPPKLE-----RHVKNIYKALDSDDEVLV 281
QY 287 RMLLTGQNLDDAFALHVAVEHCDISKYITELLDLADLVNHNPRGYTVLHIAARRREP 346
DB 282 KMLLEGHNTLDEAYALHFAIAHCAVKTAYDLELELADLVNHNPRGYTVLHVAARRKEP 341
QY 347 KIIVSLLTKGARPADVTDEGRKAVQISKRLTKOGDYFGVTEEGKPSPKDRLCIEILEQAE 406
DB 342 KLIISLUMKGANLDTLQGRALVIVKRLTKADDTYKTDGTPSLKGLCIEVLEH-E 400
QY 407 RRDPLQIG--EASVSLAMAGESLRGLLYLENVALARIMFPMEARVAMDAVQDGTLEFN 464
DB 401 QKLEYLSPIEASLSLPTVPEELRMRLYYENVALARLLFPVETETVOGIAKLEETCEFT 460
QY 465 LGSGANPPE--RQRTVDLINESPFTMKEEHLARMTALSKTVELKRFPPRCNSVLDKTM 522
DB 461 -ASSLEPDHIGKRTSLDNLNAPFOIHEKHLISRLALCKTVELKRYKRCGS--LDHFM 517
QY 523 DDE--TDPVSLGRDT--SAEKRRPHDLQVLOKAFHEDKEENDRSGLSSSSSSTISGA 577
DB 518 DTEDLNHLASVEDTPEKRLQKQRYMELQETLMKTFSEDKEE---CGKSSPKPKPTS--A 572
QY 578 IRPRR 582
DB 573 VRSNR 577

RESULT 4
Q9FHE3 PRELIMINARY; PRT; 593 AA.

Q9FHE3;
AC 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE REGULATORY PROTEIN NPRI-LIKE, TRANSCRIPTION FACTOR INHIBITOR I KAPPA B-LIKE.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RT Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty p1 and TAC
RT clones.";
RL DNA Res. 7:31-63(2000).
DR EMBL; AB019224; BAB09496.1; -;
SQ SEQUENCE 593 AA; 66833 MW; 5AD457E04DC63693 CRC64;

Query Match 34.3%; Score 1012.5; DB 10; Length 593;
Best Local Similarity 40.9%; Pred. No. 5.5e-62;
Matches 244; Conservative 100; Mismatches 192; Indels 61; Gaps 14;

QY 9 TNAFSDSDSASVEEGDADADADVEALRRLLSDNLAARSPF-DFAFLADARAVPGGGG 67
DB 25 SNHFSSSASNP-----VVSFLKLSNLEQLLSNSDCDY---SDAEIIVDVPVG 72
QY 68 GGDRLVHRCVLSARSFPLRGVFAARRAAAGGGGEGDSERLERLRELLGGGEEVGVYE 127
DB 73 -----VHRCILAAKSFQDLFKKKEKIS-----KTEKPKYQUREMLPYGA-----VAHEA 118
QY 128 LRLVLDYLSGRVGDLPKAAACLCVDEDAHVCHCPAVAFMAQVFAAFTQVAELTNLFQ 187
DB 119 FLYFLSYITGRKLPPELVSTCVDPVCSHDCRPAIDFVQVLMYASSVQVPELVSSQ 178
QY 188 RRLDVLKVEVDNLLILSVANLCNCKMKLLERCLDMVVRNLDMTLEKSLPPDVTK 247
DB 179 RRLCNFEVTLVENVLPILMVAFNCKLT--QLLDQCIERVARSRLYRFCIEKEVPEVAE 236
QY 248 QIIDARLGLISPEKNGFPNK-----HVRIHRLDSDDEVLVRLMLLTGQTNLDDA 300
DB 237 KIKQLR---LISPQDEETSPKISEKLLERIGKILKALDSDDEVLKLLITSDITLQQA 292
QY 301 FALHVAVEHCDISKITTELDDLADLVNHNPRGYTVLHIAARRREPKIIVSLLTKCARPA 360
DB 293 NGLHYSVVYSDPKVVAEILALDMDGVNRSRGYTVLHFAAMRREPSIILSIDKGNAS 352
QY 361 DVTFDGRKAVQISKRLTKOGDYFGVTEEGKPSPKDRLCIEILEQAEARRDPQLGEASVSLA 420
DB 353 EFTSDGRSAVNILRLTNPKDYHTKTAKGRESSKARLCIDILEREIKKNPMVLDTMCSI 412
QY 421 MAGESLRGLLYLENVALARIMFPMEARVAMDAVQDGTLEFNLCSGANPPE---ROR 477
DB 413 SMPEDLQMLLLEKRVGLAQLFPTPEAKVAMDIGNVEGTSEF---TGLSPSPSSGLTGNL 469
QY 478 TTVDLINESPFTMKEEHLARMTALSKT-----VELGKRFPPRCNSVLDKIM-----DDE 525
DB 470 SQVDLNETPHMQTORLLTRWALMTKGNKLLALFEGRFRFPYGVSEVLDKYMAYETDDI 529
QY 526 TDPVSLGRDTSAB---KKRFHDLQVLOKAFHEDKEENDRSGLSSSSSSTISGAIR 579
DB 530 LDDFHEKGSTHERRLKRMRYRELKDDVQKAYSKOKESKIARSLASASSPSSSSIR 586

RESULT 5
Q9FHE3 PRELIMINARY; PRT; 601 AA.


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Db 289 SREVVKALLEGAADVNYVAGPTGKLTALHIAAEMVSPDMVAVLLDHDHDPNVQTVDTGTP 348
QY 370 VOISKRLTK-----QGDYFGVTEGKPSKDRLCIEILEQA-----ERRD----- 409
Db 349 LDILRTLTDFLFGAIGLTHI-EPN-KLRCLCLELVQSAALVIREEGNNNSNDNTMI 406
QY 410 -POLGEASVSLAMAGESLRLLYL 433
Db 407 YPRMKDEHTS-----GSSLDLSRLVYL 427

RESULT 7
Q92VC2 PRELIMINARY; PRT; 491 AA.
AC Q92VC2;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE F13H10.8 PROTEIN.
GN F13H10.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; euroids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
RA Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
RA "Arabidopsis thaliana chromosome II BAC F13H10 genomic sequence.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005662; AAC78536.1; -
DR InterPro; IPR00210; -
DR InterPro; IPR002110; -
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF00651; BTB; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50097; BTB; 1.
DR SMART; SM00248; ANK; 1.
SQ SEQUENCE 491 AA; 54001 MW; F2B8A7133B591776 CRC64;

Query Match 14.3%; Score 421; DB 10; Length 491;
Best Local Similarity 29.2%; Pred. No. 3.6e-21;
Matches 135; Conservative 72; Mismatches 170; Indels 86; Gaps 15;

QY 32 EALRLRLS---DNLAFAFRSPEDFAFLADARIAVPGGGGGDLRHVRHCVLSARSFPLRGV 88
Db 6 ESLSRLSLDFNLINGQAFSDVTSVEGR-----VHAHRCILARSLEFFK 54
QY 89 FARRAAAAGGGGDSERLELRLGGGGEV-----EYGEALRLVYL 132
Db 55 FC-----GTDSPQPVGTGIDPTQHGSPASPTRGSTAGAPIVNSVGYEVLLEL 104
QY 133 DYLSGRVGDLP---KAACLVDEDCAHVCHPAVAFMAQVFASTFOVLETLNLFQR 189
Db 105 QFLYSGQSVIPQKHEPRNCGERCWHTHCSAAVDLADLTAAASRYFVEQALLTQKQ 164
QY 190 LLDVLDKVBDVNDLLLSVANLCNCKMLERCLDMVVRSLDMLTLEKSLPPDVVVKOI 249
Db 165 LASWKEKASIDRSLPHNNHHHDLSSVAQDLEQKIRRMRLDSSDVELYKLVMGEGNL 282
QY 250 IDARLSLGL-----ISPEN-----KGFNKHVRIHRLALSDSDVELYMLLTGQTNL 297
Db 223 EELRLKSSSTARSLPHNNHHHDLSSVAQDLEQKIRRMRLDSSDVELYKLVMGEGNL 282
QY 298 DDAFALHYAVEHCDKITTLELDDALADVNH--RNPRGYTVLHIAARRRPFKIVSLLTGK 356
Db 283 DESLALHYAVESCSREVVKALLEGAADVNYVAGPTGKLTALHIAAEMVSPDMVAVLLDHDH 342

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QY 357 ARPADVTFGRKAVOISKRLTK-----QGDYFGVTEGKPSKDRLCIEILEQA----- 405
Db 343 ADPNVTVGGITPLDLRLTSDTFLFKGAVPGLTHI-EPN-KLRCLCLELVQSAAMVIRE 400
QY 406 -----ERRD-----POLGEASVSLAMAG--ESLRGLLYL 433
Db 401 EGNNSNNQNDNTGTIPHMNEHNSGSGSGNNNLDLSRLVYL 443

RESULT 8
Q9VXM6 PRELIMINARY; PRT; 993 AA.
AC Q9VXM6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE CG16952 PROTEIN.
GN CG16952.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.B.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Frannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA De Pablos B., Deicher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flosser C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Gloder A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaitali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinscock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003500; AAF48532.1; -
DR FlyBase; FBgn0030701; CG16952.
DR InterPro; IPR000210; -
DR Pfam; PF00651; BTB; 1.
DR PROSITE; PS50097; BTB; 2.
DR SMART; SM00225; BTB; 1.
SQ SEQUENCE 993 AA; 108604 MW; B62CF6E625BAD788 CRC64;

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DR DR EMBL; U50094; AAB47805.1; JOINED.
DR DR EMBL; U50095; AAB47805.1; JOINED.
DR DR EMBL; U50096; AAB47805.1; JOINED.
DR DR EMBL; U50097; AAB47805.1; JOINED.
DR DR EMBL; U50098; AAB47805.1; JOINED.
DR DR EMBL; U50099; AAB47805.1; JOINED.
DR DR EMBL; U50100; AAB47805.1; JOINED.
DR DR EMBL; U50101; AAB47805.1; JOINED.
DR DR EMBL; U50102; AAB47805.1; JOINED.
DR DR EMBL; U50103; AAB47805.1; JOINED.
DR DR EMBL; U50104; AAB47805.1; JOINED.
DR DR EMBL; U50105; AAB47805.1; JOINED.
DR DR EMBL; U50106; AAB47805.1; JOINED.
DR DR EMBL; U50107; AAB47805.1; JOINED.
DR DR EMBL; U50108; AAB47805.1; JOINED.
DR DR EMBL; U50109; AAB47805.1; JOINED.
DR DR EMBL; U50110; AAB47805.1; JOINED.
DR DR EMBL; U50111; AAB47805.1; JOINED.
DR DR EMBL; U50112; AAB47805.1; JOINED.
DR DR EMBL; U50113; AAB47805.1; JOINED.
DR DR EMBL; U50114; AAB47805.1; JOINED.
DR DR EMBL; U50115; AAB47805.1; JOINED.
DR DR EMBL; U50116; AAB47805.1; JOINED.
DR DR EMBL; U50117; AAB47805.1; JOINED.
DR DR EMBL; U50118; AAB47805.1; JOINED.
DR DR EMBL; U50119; AAB47805.1; JOINED.
DR DR EMBL; U50120; AAB47805.1; JOINED.
DR DR EMBL; U50121; AAB47805.1; JOINED.
DR DR EMBL; U50122; AAB47805.1; JOINED.
DR DR EMBL; U50123; AAB47805.1; JOINED.
DR DR EMBL; U50124; AAB47805.1; JOINED.
DR DR EMBL; U50125; AAB47805.1; JOINED.
DR DR EMBL; U50126; AAB47805.1; JOINED.
DR DR EMBL; U50127; AAB47805.1; JOINED.
DR DR EMBL; U50128; AAB47805.1; JOINED.
DR DR EMBL; U50129; AAB47805.1; JOINED.
DR DR EMBL; U50130; AAB47805.1; JOINED.
DR DR EMBL; U50131; AAB47805.1; JOINED.
DR DR EMBL; U50132; AAB47805.1; JOINED.
DR DR HSSP; Q00421; 1AWC.
DR DR InterPro; IPR000488; -.
DR DR InterPro; IPR000906; -.
DR DR InterPro; IPR002110; -.
DR DR Pfam; PF00023; ank; 22.
DR DR Pfam; PF00531; death; 1.
DR DR Pfam; PF00791; ZU5; 1.
DR DR PROSITE; PS50088; ANK_REPEAT; 20.
DR DR PROSITE; PS50297; ANK_REP_REGION; 1.
DR DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR DR SMART; SM00248; ANK; 1.
DR DR SEQUENCE 1856 AA; 203465 MW; 4A4E3A794DD6401F CRC64;

Query Match 4.88; Score 143; DB 4; Length 1856;
Best Local Similarity 23.98; Pred. No. 0.43;
Matches 76; Conservative 37; Mismatches 107; Indels 98; Gaps 12;

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RESULT	9
Q99407	PRELIMINARY; PRT; 1856 AA.
ID	Q99407;
AC	Q99407;
DT	01-MAY-1997 (TrEMBLrel. 03, Created)
DT	01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE	ANKYRIN.
GN	ANK1.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9608;
[]	
RN	SEQUENCE FROM N.A.
RA	Forget B.G., Tse W.T., Gallagher P.G., Scarpa A.L., Lux S.E. ;
RL	Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases .
DR	EMBL; U50133; AAB47805.1; -
DR	EMBL; U50092; AAB47805.1; JOINED.

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QY 459 GTLEFNLSGANPPPERQRTTVDLNEPESFIMKEELHARMTALSKTVLCKRFFPRCSNVL 518
Db 817 ELUDF-----VPLKQV-----ESPAIRP-----CAMPETVIRSEQEQASKEY 859
QY 519 DKIMDETPVSLGRDTS 536
Db 860 D---EDSLIPSPAVETS 874

RESULT 10
ID Q9U3S0 PRELIMINARY; PRT; 597 AA.
AC Q9U3S0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE C04F12.3 PROTEIN.
GN C04F12.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RN RP SEQUENCE FROM N.A.
RA Lloyd C.R.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; Z81461; CAB62796.1; -.
DR HSSP; P42773; 1IIB.
DR InterPro; IPR000488; -.
DR InterPro; IPR002110; -.
DR Pfam; PF00023; ank; 6.
DR Pfam; PF00531; death; 1.
DR PROSITE; PS50088; ANK_REPEAT; 4.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR SMART; SM00248; ANK; 1.
SQ SEQUENCE 597 AA; 66421 MW; CD271B6B4CF25A35 CRC64;

Query Match 4.8%; Score 140.5; DB 5; Length 597;
Best Local Similarity 20.1%; Pred. No. 0.12;
Matches 107; Conservative 92; Mismatches 202; Indels 131; Gaps 23;

QY 73 VHRCVLSARSPFLRGVFAARRA-----AAGGGEDGSRLELRELLGGGEEVGYEA 127
Db 32 IHKSSQHRRLFIDDTISTEASAGDRWATCAGAGATELTIHFL---GDQFEESAIDV 88
QY 128 LR---LVLDYLSGRVGLPKAACLCVDECAHVGHCPAVAFMAQVLFAASTFQVAELTN 184
Db 89 VRKHSVMFTVPS-----LKVDS-----LEVELRESTNDNVTTISF 126
QY 185 LFQRLDLVDLKVQV---DNLLILSVANLCKNSCKMLLERCLDMVVRNLDMT----- 236
Db 127 KYLPRIQSRSHTEISLDFNLLEFAT-----NGDTISLLQPFVAQISKQDIEGTVFHYA 181
QY 237 -----LEKSLPPDVIKQIDARLSLGLISPENKGFPHKVRRIHRLALSDSDVEL 285
Db 182 ANKQSFSLKLLSVIPDDIKNEVINQNHGLTA-----LHVAIRTGDDPA 228
QY 286 VRMLTPEG-QTNLDD---AFALHYAVEHCDSKITTELLDLALA---DVNHRNPRGYTVLH 338
Db 229 VHYLMNHGAKIDISDNHGSTALHYLGDAYNESIFKLEILEPSCQRQFDVQLNSEGAPIH 288
QY 339 IAARRREPKIIVSLTKGARPADVT- DGRKAVQISKRTKQGDYFGVTEEGKPSKPKDL 397
Db 289 VAVRRLKLSLIEALGAL---IDFLDTKKRNALHAIEMNDFETI-----QL 335
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QY 398 CJEILLEQAEERDPOLGEASVSLAMAGESLRGRLLYLNRVALARIMFPPEARVAMDIQV 457
Db 336 LVERGSGTNIED-ESGETALSLAVKNVNPVYIGLLDNGADPNR-----ONSKGICLADS 389
QY 458 DGTLEFNLSGANPP-PERQRTTVD-----LNESPFT-----MKE 491
Db 390 EDSVONIINGDRPELPKKEAFGVPNDLAISRPLFGSRHSDPQAPGEEGRHVRKRSRE 449
QY 492 EHL-ARMTALSKTVLKGKRRFFPCSNVLDKIMDETPVSLGRDTSARKKR 542
Db 450 ETLNDAQTLLETDSMA-----PRVSRISTSESEDOQP---GPSTSSGTRRR 494

RESULT 11
ID Q9FRM5 PRELIMINARY; PRT; 265 AA.
AC Q9FRM5;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE PUTATIVE ANKYRIN PROTEIN.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae;
OC Oryza.
OX NCBI_TaxID=4530;
RN [1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,
RA Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSJNBa0056G17 genomic sequence."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC018727; AAG46181.1; -.
SQ SEQUENCE 265 AA; 27930 MW; BFCA48939F8B0200 CRC64;

Query Match 4.6%; Score 135.5; DB 10; Length 265;
Best Local Similarity 19.8%; Pred. No. 0.084;
Matches 75; Conservative 37; Mismatches 88; Indels 179; Gaps 11;

QY 63 GGGGGGDLRVHRCVLSARSPFLRGVFAARRAAGGGEDGSRLELRELLGGGEEVE 122
Db 6 GGGGGGG-----GGRGGRGR-----GGGEEDD 29
QY 123 VGYEALRLVLDYLY-SGRVGLPKAACLCVDECAHVGHCPAVAFMAQVLFAASTFQVAE 181
Db 30 L-----HLHKAARSGDLAAESLC----- 48
QY 182 LTNLFORLLVDLKVQVNDNLLILSVANLCKNSCKMLLERCLDMVVRNLDMTLEKSL 241
Db 49 -----EANPLAL-----NSRDLRSRTPL----- 66
QY 242 PPDVIKQIIDARLSLGLISPENKGFPHKVRRIHRLALSDSDVELVRLMTE---GOTNL 297
Db 67 -----HLAAGHVELVKCLCKHKHADVGAAM 93
QY 298 DDAFALHYAVEHCDSKITTELLDALADVNRHNRNPRGYTVLHIAARRREPKIIVSLTKGA 357
Db 94 DDTAAIHFAFSQKHGVVRELL-ASGASVKAKNRKGFTALHFASQNSHLELVLYLVKGA 152
QY 358 RADVTFDGRKAVQISKR-----LTKQGDYFGVTEEGKPSKPKDLICILEQ 404
Db 153 DIAAKTKGQGTALHVAEKDDVDRDFLKECEQSLKKGEL-----PSEKKDDSVSTIAE 204
QY 405 AERRDPQLGEASVSLAMAG 423
Db 205 KPDDKSSGEATKDEDEAG 223
```



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RESULT 14
Q9H1Q1 PRELIMINARY: PRT: 1710 AA.
ID Q9H1Q1
AC Q9H1Q1
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE BA145E8.1 (KTA1074).
GN BA145E8.1
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL16272; CAC19649.1;
SQ SEQUENCE 1710 AA; 196410 MW; 01CBF9BADB894872 CRC64;

Query Match 4.6%; Score 135; DB 4; Length 1710;
Best Local Similarity 19.4%; Pred. No. 1.4;
Matches 99; Conservative 68; Mismatches 176; Indels 166; Gaps 17;

QY 87 GVFARRAAAGGGGDSERLELRLGGGEEVEVGEALRLVLDYLSRGVGDLPKA 146
D 1111 :|||||
Db 14 GSFARRORSSAGGGEPE-----GAYSQPGYHVR----- 43
QY 147 ACLCDEDCARHVGCHPAVAFMAQVLAFASTFOVAELTNLFORRLDVLDKVVDNLLIL 206
D 1111 :|||||
Db 44 -----DRD-----LCKIHKASAGNVAKVQIILLKRLKGLNDRDKMRTALHL 86
QY 207 SVANLCNCKMCKLLERCLDMVYRSLDMTLEKSLPPDVVIKQIDARLSGLISPENKGF 266
D 1111 :|||||
Db 87 ACAN-----GHPEVTVLLVDRKCOLNVCNDENR--- 114
QY 267 PNKHVRRTHRALSDSDVELVRLMTEG-QTNLDDAF-----ALHYAVEHCDSKITTELLDLA 322
D 1111 :|||||
Db 115 -----TALMKAVQCEKATILLEGADPNLADVHGNLTHYAVINEDISVATKLL-LY 168
QY 323 LADVNRNPRGTVLHIAARRREPILVSLTRKGPADVTFDGRKAVQISKRLTKQGDY 382
D 1111 :|||||
Db 169 DANIEAKNKDDLTPLLAVSGKKQVVEFLIKKA----- 203
QY 383 FGVTEGKPSKDRLCIELEQARRDPOLGEASVSLAMAGESLGRLLYLENRVALARI 442
D 1111 :|||||
Db 204 -NVNAVVKLESSHQLITSEYKE--ERIPKHSQNSNSVDESSEDSLSRL----- 248
QY 443 MFPMEARVAMDTA-----QVDGTLEFNLGSGANPPPERQRTVDLNSPFTMKEEHARMTA 499
D 1111 :|||||
Db 249 -----SGKPGVDDSWPTSDDEDLNFTKNVPKPSLAKLMTA-----SQQSRKNLEA 294
QY 500 LSKTVELGKR--FFPRCSNVLDKIMDETDPVSLGRDTSAEKKRKF-----HDLQDVLOKA 553
D 1111 :|||||
Db 295 TYGTVRTGRTLFEDRDSQDEVVVESLPTTSI-----KVQCFSHPTYSPLDLPKP 347
QY 554 FHED-----KEENDRSGLSSSSSSTSI 575
D 1111 :|||||
Db 348 SHKSLANPGLMKEEPTKPGIAKKENGIDI 376

RESULT 15
Q9VT60 PRELIMINARY: PRT: 877 AA.
ID Q9VT60
AC Q9VT60
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE CG6718 PROTEIN.
GN CG6718.

Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BERKELEY;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpén G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinart K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J., Yang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Rao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao X., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003550; AAF50194.1; -.
DR FLYBase; FBgn0036053; CG6718.
DR FlyBase; FBgn0036053; CG6718.
DR InterPro; IPR002110; -.
DR InterPro; IPR002641; -.
DR Pfam; PF00023; ank; 5.
DR Pfam; PF01734; Patatin; 1.
DR PROSITE; PS50088; ANK_REPEAT; 3.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR SMART; SM00248; ANK; 1.
SQ SEQUENCE 877 AA; 96862 MW; C9DC2CD6C282869B CRC64;

Query Match 4.5%; Score 133.5; DB 5; Length 877;
Best Local Similarity 20.2%; Pred. No. 0.66;
Matches 92; Conservative 63; Mismatches 167; Indels 133; Gaps 19;

QY 189 RLVDLDKVEVDNLLILSLVANLCKNCKMLERCLDMVYRSLDMTLEKSLPP 243
D 1111 :|||||
Db 141 KMLQCVQDAATLMSPFOLA--IKQGHMEVKKALLPLSKLEHLDINSNSVFHYAATTK 198
QY 244 DVIKQIIDARLSGLISPENKGFNKHVRRIHRLDSDSDVELVRLMTEG----- 293
D 1111 :|||||
Db 199 EIINLIID-KSTVNLNHLNSDGYTPLHV-----ACLADKPNVKKALLAGANVNLAKDI 252
QY 294 -----QTNLDDAF-----LHYAVEHCDSKITTELLDALADVNH 328

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Db 253 RKVYKTSAPTTSFLRTNVSKLYTQDMKYGGTPLHW---CSSRETLHALINEGCDVNA 308
Qy 329 RNPGRYTVLHIAARRRREPKIIVSLITKGARPADVTFDGRKA--VOISKRLTKOGD---YF 383
Db 309 TNFDGRTALHVMVARNRFEQVVTLLAHDAEIDVLDKDGNAALHIALEKLVPIVQCLVWF 368
Qy 384 GVTEEGKPSKDRLCIILSQARRDPQLGEASVSLAMAGESLRG---RLLYLENRVAL 439
Db 369 G-----CDINLNKKGKTPR-----HMGNDASGNKDDIELYLHLSVGA 407
Qy 440 ARIMFPMEARVAMDIQVDTGLEFNLGSGANP-----PPERQRTTVDLNESPFI 488
Db 408 KRCK-----DTGSKCPCPGCNAGKNGYNGIPPEAPES-----V 438
Qy 489 MKEEHLARMTALSKTVELGKRFFPRCSNVLDKIMDDETDPVSLGRDTSAEKRRPHLQD 548
Db 439 EOREHIEHMLATTSRQMMGGFLNAAANGILEK-QQPAQKPVV--DT--EKELKGQSIMD 493
Qy 549 VLQKAF-----HEDKEENDRSGLSSSSSTSIGA 577
Db 494 ALLGMFTTKVNADMKKENSDDLASGSKSAYSS 528

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Search completed: July 12, 2001, 17:14:33
Job time: 115 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 12, 2001, 17:12:38 ; Search time 22.27 Seconds
(without alignments)
1584.336 Million cell updates/sec

Title: US-09-294-539-4
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Sequence: 1 MEPTSHVTNAFSDSDASV.....RSLGSSSSSTSGAIRPRR 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2952	100.0	582	22	Rice NPR1 homologue
2	2910	98.6	578	21	Rice putative nega
3	1737	58.8	576	21	L. esculentum NIM1
4	1672.5	56.7	588	19	Nicotiana glutinos
5	1672.5	56.7	588	21	N. tabacum NIM1 ho
6	1629	55.2	604	21	B. vulgaris NIM1 h
7	1285	43.5	593	21	Arabidopsis thalia
8	1276	43.2	593	19	A. thaliana NIM-1
9	1276	43.2	593	19	Arabidopsis thalia
10	1276	43.2	593	19	Arabidopsis thalia
11	1272	43.1	593	19	A. thaliana non-in

12	1270	43.0	593	19	AAW64436	A. thaliana varian
13	1270	43.0	593	19	AAW61983	Non-inducible immu
14	1222.5	41.4	579	21	AAW27303	B. napus NIM1 homo
15	1213.5	41.1	600	21	AAW27307	A. thaliana NIM1 h
16	1213.5	41.1	601	21	AAW27328	A. thaliana NIM1 h
17	1188.5	40.3	521	19	AAW64438	A. thaliana C-term
18	1188.5	40.3	521	19	AAW61985	Non-inducible immu
19	1134	38.4	469	19	AAW64437	A. thaliana N-term
20	1134	38.4	469	19	AAW61984	Non-inducible immu
21	1087	36.8	621	21	AAW36271	Maize NPR1 transla
22	1087	36.8	621	21	AAW36272	Maize NPR1 transla
23	1060.5	35.9	591	21	AAW27325	H. annuus NIM1 homo
24	1052.5	35.7	397	19	AAW64439	A. thaliana C- and
25	1052.5	35.7	397	19	AAW61986	Non-inducible immu
26	1045.5	35.4	609	22	AAW48088	Wheat Nph2-2 prote
27	1045	35.4	607	22	AAW48087	Wheat Nph2-1 prote
28	1043	35.3	427	21	AAW17534	Arabidopsis thalia
29	1031	34.9	586	21	AAW27304	A. thaliana NIM1 h
30	1031	34.9	586	21	AAW41887	Arabidopsis thalia
31	1009	34.2	574	21	AAW27327	A. thaliana NIM1 h
32	995	33.7	475	22	AAW48086	Rice Nph1 protein.
33	987	33.4	455	22	AAW09876	Rice putative nega
34	971.5	32.9	601	21	AAW27306	A. thaliana NIM1 h
35	946.5	32.1	479	21	AAW41888	Arabidopsis thalia
36	904	30.6	377	21	AAW17535	Arabidopsis thalia
37	844.5	28.6	409	22	AAW48093	Protein encoded by
38	842.5	28.5	425	21	AAW41889	Arabidopsis thalia
39	825	27.9	217	21	AAW27316	S. tuberosum NIM1
40	823	27.9	219	21	AAW27308	Arabidopsis thalia
41	782.5	26.5	381	22	AAW48091	N. tabacum NIM1 ho
42	751	25.4	261	19	AAW64440	Putative protein e
43	751	25.4	261	19	AAW61987	A. thaliana NIM-1
44	739	25.0	325	21	AAW09874	Non-inducible immu
45	678	23.0	369	21	AAW27329	Corn negatively ph
						N. tabacum NIM1 ho

ALIGNMENTS

RESULT 1
AAB29750
ID AAB29750 standard; Protein; 582 AA.
XX
AC AAB29750;
XX
DT 28-FEB-2001 (first entry)
XX
DE Rice NPR1 homologue 1 (NIM1), SEQ ID NO:4.
XX
KW Rice; NIM1; NPR1 homologue 1; PNI Interactor; SAR; bZIP protein;
KW systemic acquired resistance; yeast two-hybrid system; transgenic plant;
KW pathogen resistance; virus; bacterium; nematode; fungus; insect.
XX
OS Oryza sativa.
XX
PN WO200063417-A2.
XX
PD 26-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US09060.
XX
PR 19-APR-1999; 99US-0294539.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Chern MS, Ronald P;
XX
DR WPI: 2001-090867/10.
XX
DR N-PSDB; AAC81457.
XX
PT Novel nucleic acid construct for enhancing pathogen resistance, encodes
PT rice proline rich NPR1 interactor proteins, polypeptides interacting
PT with PNI or MNI, and bZIP protein interacting with Arabidopsis NPR1

xx The invention relates to rice proteins (AAB29749-B29757) and the
ps nucleotides encoding the proteins (AAC01456-C01464), which are involved
cc in the induction of systemic acquired resistance (SAR), a general plant
cc resistance response that can be induced during a local infection by an
cc avirulent pathogen. A rice cDNA library was screened using the yeast two
cc hybrid system with Arabidopsis NPR1 cDNA as bait, and the rice proteins
cc PNI (proline rich NPR1 interactor; AAB29749) and MNI (AAB29758) were
cc identified as interacting with Arabidopsis NPR1. The rice cDNA library
cc was then rescreened using rice PNI cDNA or rice MNI cDNA as bait. Rice
cc NH1 and NH2 (NPR homologues 1 and 2; AAB29750, AAB29751), nucleolin-like
cc protein (AAB29752), PREG-like protein (AAB29753), and a protein with no
cc known homology (AAB29754) were identified as interacting with PNI
cc protein, and rice GRL1 and GRL2 (glutaredoxin homologues 1 and 2;
cc AAB29755, AAB29756) and rice MAP1A (a protein with homology to rat
cc microtubule-associated protein; AAB29757) were found to interact with
cc rice MNI protein. The invention additionally encompasses transgenic
cc plants comprising an expression cassette encoding a protein of the
cc invention, and a method for enhancing resistance to pathogens in a plant
cc by introducing the expression cassette into the plant, and selecting the
cc plant with enhanced resistance. The rice SAR-associated nucleic acids and
cc proteins are useful for enhancing plant resistance to pathogens such as
cc viruses, bacteria, nematodes, fungi or insects. The present sequence
cc represents rice NH1.
xx
SQ Sequence 582 AA;

Query Match 100.0%; Score 2952; DB 22; Length 582;
Best Local Similarity 100.0%; Pred. No. 7.6e-277;
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEPTSHVTNFAFSDSASVEEGDADADADVEALRRSLDNLAARSPEDFAFLADARIA 60
Db 1 meptshvtnafdsdsasveegdadadadvealrrisdnlaaafsrpedfafladaria 60
Qy 61 VPGGGGGDLVHRCVLSARSPLRGVFAARRAAAAGGGGDSERLELRELLGGGEE 120
Db 61 vpgggggdvlhrcvlsarsplrgvfarraaaaaggggdserlelrellgggee 120
Qy 121 VEVGYEARLRLVLYSGRVDLPKAAACLCVDEDCAHVGHCPAVAFMAQVLFPAASTFQVA 180
Db 121 vevgyearlrlvlysgrvdplkaacclcvdedcahvghcpavafmaqvlfaastfqa 180
Qy 181 ELTNLFQRLLDLVDKVEVDNLLILSVANLCNCKMLLERCLDMVRSNLDMLTLEKS 240
Db 181 eltnlfqrrlldvdkvevdnllilsvanlcnckmllercldmvrslndmltleks 240
Qy 241 LPPDVIKOIIDARLSGLISPENKGFNPKHVRRIHRAALSDVVELVRLMLTEGOTNLDDA 300
Db 241 lppdvikoidarlsglispenkfgpnkhvrrihraalsdvdvrlmltegotnldda 300
Qy 301 FALHYAVEHCDSKITTELLDALADVNRHNPGRYTVLHIAARRREPKIIVSLITKGARPA 360
Db 301 falhyavehcdskittelldaladvnrhnpgrytvlhiaarrrepkliivslitkgarpa 360
Qy 361 DVTDFGRKAVOISKRLTKOGDYFGVTEGKPSKPKDRICIELEOARERDPOLGEASVSLA 420
Db 361 dvtdfgrkavoiskrltkogdyfgvteegkpskpkdricieleoaerdpolgeasvsla 420
Qy 421 MAGESLRGRLLYLENRVALARIMFMEARVAMDIQAQVDTGLEFNLGSGANPPPQRQTIV 480
Db 421 mageslrgrrllylenrvalarimfmearvamdiqaqvdtglefnlgsganppqrqtiv 480
Qy 481 DLNESPFTMKEEHLARMTALSKTVELGRFPPRCNSVLDKIMDETDPVSLGRDTSABKR 540
Db 481 dlnespftmkeehlarmtalstvelgrfpprcnsvldkimmddetpvsigrdtsabkr 540
Qy 541 KRFHDLQDLQKAFHEDKEENDRSGLSSSSSSTSTIGAIRPRR 582
Db 541 krfhdlqdlqkafhedkeendrsghlssssststigairrrr 582

RESULT 2

xx AAB09875
ID AAB09875 standard; Protein; 578 AA.
xx AC AAB09875;
xx DT 12-OCT-2000 (first entry)
xx DE Rice putative negatively phytochrome regulated 1 (NPR1) gene product #1.
xx KW Rice; negatively phytochrome regulated 1 gene; NPR1;
xx KW systemic acquired resistance; gene mapping; transgenic plant.
xx OS Oryza sativa.
xx SN WO200028036-A2.
xx PD 18-MAY-2000.
xx PF 04-NOV-1999; 99MO-US25953.
xx PR 05-NOV-1998; 98US-0107242.
xx PA (DUPO) DU PONT DE NEMOURS & CO E I.
xx PI Famodu OO, Fang Y, Liu Z, Miao G, Odell JT;
xx DR WPI; 2000-451636/39.
xx DR N-PSDB; AAA61047.
xx PT Isolated nucleic acid fragments encoding an NPR1 gene which can be used
xx PT to transform plants and provide disease resistance
xx PS Claim 1; Page 29; 35pp; English.
xx CC The present sequence is the product of a putative version of the corn
xx CC negatively phytochrome regulated 1 (NPR1) gene. Its coding sequence was
xx CC isolated by screening a leaf cDNA library for those sequences
xx CC which were similar to the NPR1 gene from Arabidopsis thaliana. This
xx CC protein is involved in systemic acquired resistance and its gene can be
xx CC used to create transgenic plants which are protected from pathogens. It
xx CC can also be used to find homologous sequences in other plants which have
xx CC a similar effect.
xx SQ Sequence 578 AA;
Query Match 98.6%; Score 2910; DB 21; Length 578;
Best Local Similarity 99.5%; Pred. No. 8.7e-273;
Matches 575; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5 TSHVTNFAFSDSASVEEGDADADADVEALRRSLDNLAARSPEDFAFLADARIAVPGG 64
Db 1 tshvtnafdsdsasveegdadadadvealrrisdnlaaafsrpedfafladariavpvg 60
Qy 65 GGGGGDLVHRCVLSARSPLRGVFAARRAAAAGGGGDSERLELRELLGGGEEVEVG 124
Db 61 gggggdvlhrcvlsarsplrgvfarraaaaaggggdserlelrellgggeevvg 120
Qy 125 YEALRLVLYSGRVDLPKAAACLCVDEDCAHVGHCPAVAFMAQVLFPAASTFQVAELTN 184
Db 121 yealrlvlysgrvdplkaacclcvdedcahvghcpavafmaqvlfaastfqaelt 180
Qy 185 LFORLLDLVDKVEVDNLLILSVANLCNCKMLLERCLDMVRSNLDMLTLEKSLPPD 244
Db 181 lforlldvdkvevdnllilsvanlcnckmllercldmvrslndmltlekslppd 240
Qy 245 VIKOIIDARLSGLISPENKGFNPKHVRRIHRAALSDVVELVRLMLTEGOTNLDDAFALH 304
Db 241 vikoidarlsglispenkfgpnkhvrrihraalsdvdvrlmltegotnlddafaalh 300

305	QY	YAVEHCDSKITTELLDLALADVNHRNPRGYTVLHIAARRREPKIIVSLTKGARPADYTF	366
301	Db	yavehcdskittelldlaladvnhrnprgytvLhiaarrrePKIIVSLITKgarpadvtf	360
365	QY	DGRKAVQIISKRLTKOGDYGVTEEGKPSPKDLRCIEILEQAERRDPQLGEASVSLAMAGE	424
361	Db	dgrkavqiskrltkcgdygvteegkpspkdrlcieileqearrpdqLgeasvsLamAge	420
425	QY	SLRGRLLYLENRVALARIMFPMEARVAMDIADVDGTFLENLGSGANPPPERQRTTVDLNE	484
421	Db	slrglllylenrvalarimfpmearvamdiagvdtlefnlgsganppperqrttvdline	480
485	QY	SPIMKEEHLARMTALSKTVELGKRFPPRCNSVLDKIMDDTDVPSLGRDTSAEKRRKRP	544
481	Db	spfmkeeHLarMTalsktvElgrffrcsnvldkimddtdpvsLgrdtSaeKrrkrfh	540
545	QY	DLQDVQLQKAFHEDKEENDRSGLSSSSSTSGAIRPRR	582
541	Db	dldqvlgkafhedkeendrsglssssstsgairpr	578
RESULT	3		
AAB27302			
ID	AAB27302	standard; Protein; 576 AA.	
XX	AAB27302;		
XX	AC		
XX	AC		
DT	25-JAN-2001	(first entry)	
XX			
DE	L. esculentum NIM1 homologue SEQ ID NO: 4.		
XX			
KW	Systemic acquired resistance; SAR; signal transduction cascade;		
KW	disease resistance; tobacco; tomato; canola; sunflower; sugarbeet;		
KW	potato.		
XX			
OS	Lycopersicon esculentum.		
XX			
PN	WO200053762-A2.		
PD			
PD	14-SEP-2000.		
XX			
PF	07-MAR-2000; 2000WO-EP01978.		
XX			
PR	09-MAR-1999; 99US-0265149.		
XX			
PA	(NOVS) NOVARTIS AG.		
PA	(NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.		
XX			
PI	Salmeron JM, Weislo LJ, Willits MG, Mengiste T;		
XX			
DR	WPI; 2000-594322/56.		
DR	N-PSDB; AAA97191.		
XX			
PT	Novel plant genes for enhancing systemic acquired resistance gene		
PT	expression and broad spectrum disease resistance in plants, are		
PT	homologues of Arabidopsis NIM1 gene -		
XX			
XX	Claim 1; Page 75-77; 152pp; English.		
XX			
CC	The present invention is concerned with the isolation of NIM1 homolog		
CC	and their coding sequences from Arabidopsis thaliana, Brassica napus,		
CC	Nicotiana tabacum, Lycopersicon esculentum, Beta vulgaris, Helianthus		
CC	annuus and Solanum tuberosum. NIM1 is one of the proteins involved in		
CC	signal transduction cascade leading to systemic acquired resistance (
CC	in plants. This gives the plants an increased resistance to disease.		
CC	protein and gene can be used to produce transgenic plants resistant t		
CC	diseases caused by viruses, such as tobacco or cucumber mosaic virus,		
CC	ringspot virus, pelargonium leaf curl virus, red clover mottle virus,		
CC	tomato bushy stunt virus, fungi, including Phytophthora parasitica a		
CC	Pernonospora tabacina, bacteria such as Pseudomonas syringae and P.		
CC	tabaci, insects, including aphids and lepidoptera and nematodes such		
CC	Meloidogyne incognita. In particular they can be used against disease		
CC	organisms of maize.		

```

PR 10-JAN-1997; 97US-0035166.
XX (GEO) GEN HOSPITAL CORP.
PA (UYDU-) UNIV DUKE.
XX Ausubel FM, Cao H, Dong X, Glazebrook J;
XX WPI; 1998-159458/14.
XX N-PSDB; AAV16852.
XX New isolated plant acquired resistance polypeptide gene - useful
PT for, e.g. producing plants with increased resistance to pathogens
PT such as bacteria
XX
XX Claim 26; Fig 7; 127pp; English.
XX
XX The sequence is that of encoded by a homologue of the acquired
CC resistance gene NPRI. Transgenic cells which produce such a
CC protein are useful in the production of plants having
CC an increased level of resistance against disease caused
CC by plant pathogens, e.g. bacteria, mycoplasmas, fungi, insects,
CC nematodes, viruses, and viroids.
XX
XX Sequence 588 AA;

Query Match 56.7%; Score 1672.5; DB 19; Length 588;
Best Local Similarity 56.8%; Pred. No. 5.4e-153;
Matches 336; Conservative 102; Mismatches 119; Indels 35; Gaps 8;

Qy 11 AFSDSDSASVEE-----GDADADADVEALRLRLSDNLAFAF-RSPEDFAFLAD 56
Db 7 afdsndisgssiccggtteffspetspaetsikrlsetiesifdaslpefyfad 66

Qy 57 ARIAPVGGGGDLRVHRCVLSARSPLRGVFARRAAAGGGGEGDSERLERELLGG 116
Db 67 akllv---sgpkelpvhrclarspffknlf-----gkknsskvelkvm-- 113

Qy 117 GGEVEVEYEAALRLVLYSGRYGDLPKAACLCVDECAHVGHCHPAVAFNAQVLF 176
Db 114 --kehevsydavmsvlaylysgkvrpskdvccvndcshvacrpavafivevlytsft 171

Qy 177 FOVAELTNLFORLLDVKVEVDNLLILSVANLCKNSCKMLERCLDMVVRNLDMIT 236
Db 172 fqiselvdkfqrhlldlkdtaadvmvlsvanicgkacerllssciefiivksnvdit 231

Qy 237 LEKSLPPDVIKQIIDARLSGLISPENKGFNKHVRRTHRALDSDVVELVRLMTEG 296
Db 232 ldkalpdhivkqitdsraeqlqpsngfpkdvkrhraldsdvvelqllreghttt 291

Qy 297 LDDAFALHYAVEHCDSKITTELLDLALADVNRNPRGTYVLHIAARRRPEKIIVSL 356
Db 292 lddayalhyavaycdakttaelldaladinhqnsrgyvtlvhvaamrkepkivvsltkg 351

Qy 357 ARPADVTEDGKAVQISKRLTKQDYGCVTEGKPSKDRICIELEQAEERDPQLGEAS 416
Db 352 arpsditsdgrkaiqrklrlvdfkspeegksasndricieleqaeerrdpqlgeas 411

Qy 417 VSLMAGESLGRLLYLENVALARIMPEARVAMDAQVDGTLFEFLNLSGANPPPERQ 476
Db 412 vslmagadllrmklllylenrvglakllfpmeakvamdiagvdtseiflasigkmanaq 471

Qy 477 RTVDNLNESPFTIMKEELHARMTALSKTVELGKRFPPRCNSVLDKIM--DDTDPVSLGRD 534
Db 472 rttvdnlneapfkkeehlnrlalsrtvelgkrfpprcsevlnkimdaddlseiyagnd 531

Qy 535 TSAE---KRRKRFHLDQVQLQAFHDEKRENR-SGLSSSSSSSTSGAIRPPR 582
Db 532 taeeqrklqymelqelktaftedkeydktnnissscsstskgvdnpknk 583

RESULT 5
AAB27301

```

```

ID AAB27301 standard; Protein; 588 AA.
XX
XX AAB27301;
XX
XX 25-JAN-2001 (first entry)
XX
XX N. tabacum NIM1 homologue SEQ ID NO: 2.
XX
XX Systemic acquired resistance; SAR; signal transduction cascade;
KW disease resistance; tobacco; tomato; canola; sunflower; sugarbeet;
KW potato.
XX
XX Nicotiana tabacum.
XX
XX WC200053762-A2.
XX
XX 14-SEP-2000.
XX
XX 07-MAR-2000; 2000WO-EP01978.
XX
XX 09-MAR-1999; 9905-0265149.
XX
XX (NOVS) NOVARTIS AG.
XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
XX Salmeron JM, Weislo LJ, Willits MG, Mengiste T;
XX
XX WPI; 2000-594322/56.
XX N-PSDB; AAS97190.
XX
XX Novel plant genes for enhancing systemic acquired resistance gene
PT expression and broad spectrum disease resistance in plants, are
PT homologues of Arabidopsis NIM1 gene -
XX
XX Claim 1; Page 70-72; 152pp; English.
XX
XX The present invention is concerned with the isolation of NIM1 homologues
CC and their coding sequences from Arabidopsis thaliana, Brassica napus,
CC Nicotiana tabacum, Lycopersicon esculentum, Beta vulgaris, Helianthus
CC annuus and Solanum tuberosum. NIM1 is one of the proteins involved in the
CC signal transduction cascade leading to systemic acquired resistance (SAR)
CC in plants. This gives the plants an increased resistance to disease. The
CC protein and gene can be used to produce transgenic plants resistant to
CC diseases caused by viruses, such as tobacco or cucumber mosaic virus,
CC ringpot virus, pelargonium leaf curl virus, red clover mottle virus,
CC tomato bushy stunt virus, fungi, including Phytophthora parasitica and
CC Peronospora tabacina, bacteria such as Pseudomonas syringae and P.
CC tabaci, insects, including aphids and lepidoptera and nematodes such as
CC Meloidogyne incognita. In particular they can be used against disease
CC organisms of maize.
XX
XX Sequence 588 AA;

Query Match 56.7%; Score 1672.5; DB 21; Length 588;
Best Local Similarity 56.8%; Pred. No. 5.4e-153;
Matches 336; Conservative 102; Mismatches 119; Indels 35; Gaps 8;

Qy 11 AFSDSDSASVEE-----GDADADADVEALRLRLSDNLAFAF-RSPEDFAFLAD 56
Db 7 afdsndisgssiccggtteffspetspaetsikrlsetiesifdaslpefyfad 66

Qy 57 ARIAPVGGGGDLRVHRCVLSARSPLRGVFARRAAAGGGGEGDSERLERELLGG 116
Db 67 akllv---sgpkelpvhrclarspffknlf-----gkknsskvelkvm-- 113

Qy 117 GGEVEVEYEAALRLVLYSGRYGDLPKAACLCVDECAHVGHCHPAVAFNAQVLF 176
Db 114 --kehevsydavmsvlaylysgkvrpskdvccvndcshvacrpavafivevlytsft 171

Qy 177 FOVAELTNLFORLLDVKVEVDNLLILSVANLCKNSCKMLERCLDMVVRNLDMIT 236
Db 172 fqiselvdkfqrhlldlkdtaadvmvlsvanicgkacerllssciefiivksnvdit 231

```

QY 237 LEKSLPPDVVKOIIDARLSGLISPENKGFNPKHVRIHRLDSDDELVELRMLLREGOTN 296
 Db 232 lokaiphdivkqitdsraeigqgpesngfpdkhvkrihraldsddvelqimllregntt 291
 QY 297 LDDAFALHYAVEHCHSKITTELDDALADVNHRNPRGYTVLHIAARRREPKIIVSLRTKG 356
 Db 292 ldalayhyavaycdaktaeidldaladinhqnsrgyvtlvhvaamrkepkivvslltkg 351
 QY 357 ARPADVTGDKRAVOISKRLTKQGYFGVTEBEGKSPKDRLCIEILEQAERDPOLGEAS 416
 Db 352 arpsdltadgrkalqakrltrivdfskspeegkasndricieileaeardpdlgeas 411
 QY 417 VSLMAGESLRGLLYLENRVALARIMPFMEARVAMDAQVDTLEFNLGSGANPPPERQ 476
 Db 412 vslmagaddrlmklllylenrvglakllfpmeakvamdiaqvdgtsefplasiagkmanaq 471
 QY 477 RPTVDLNSPFTMEHEHARMTALSKTVELGKRFPPRCNSVLDTM--DDETFDPSVLGRD 534
 Db 472 rttvdlnsapfkikehlnrlalrtvelgrffprcsevlmklmdaddiseiaymgnd 531
 QY 535 TSAE---KKRPHDLQDVLOKAFHEDKEENDR-SGLSSSSSSSTSGAIRPRR 582
 Db 532 taerqlkqrymeiqelltkafteedkeydktnnisccsstskgvdkpnx 583

RESULT 6
 AAB27324
 ID AAB27324 standard; Protein; 604 AA.
 AC AAB27324;
 DT 25-JAN-2001 (first entry)
 DE B. vulgaris NIM1 homologue SEQ ID NO: 64.
 KW Systemic acquired resistance; SAR; signal transduction cascade;
 KW disease resistance; tobacco; tomato; canola; sunflower; sugarbeet;
 KW potato.
 OS Beta vulgaris.
 FH Key Location/Qualifiers
 FT Misc-difference 590
 FT /label= Ser
 FT /note= "encoded by TCGTCG"
 XX WO200053762-A2.
 PN 14-SEP-2000.
 PD 07-MAR-2000; 2000WO-EP01978.
 PF 09-MAR-1999; 99US-0265149.
 PR (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX Salmeron JM, Weislo LJ, Willits MG, Mengiste T;
 DR WPI; 2000-594322/56.
 DR N-PSDB; AAA97229.
 XX Novel plant genes for enhancing systemic acquired resistance gene
 PT expression and broad spectrum disease resistance in plants, are
 PT homologues of Arabidopsis NIM1 gene -
 XX Claim 1; Page 130-131; 152pp; English.
 PS The present invention is concerned with the isolation of NIM1 homologues
 CC and their coding sequences from Arabidopsis thaliana, Brassica napus,
 CC Nicotiana tabacum, Lycopersicon esculentum, Beta vulgaris, Helianthus
 CC annuus and Solanum tuberosum. NIM1 is one of the proteins involved in the

CC signal transduction cascade leading to systemic acquired resistance (SAR)
 CC in plants. This gives the plants an increased resistance to disease. The
 CC protein and gene can be used to produce transgenic plants resistant to
 CC diseases caused by viruses, such as tobacco or cucumber mosaic virus,
 CC ringspot virus, pelargonium leaf curl virus, red clover mottle virus,
 CC tomato bushy stunt virus, fungi, including Phytophthora parasitica and
 CC Peronospora tabacina, bacteria such as Pseudomonas syringae and P.
 CC tabaci, insects, including aphids and lepidoptera and nematodes such as
 CC Meloidogyne incognita. In particular they can be used against disease
 CC organisms of maize.
 XX
 SQ Sequence 604 AA;
 Query Match 55.2%; Score 1629; DB 21; Length 604;
 Best Local Similarity 57.4%; Pred. No. 9.1e-145; Indels 44; Gaps 10;
 Matches 343; Conservative 81; Mismatches 130;
 QY 11 AFSDSDSAS-----VEEGDADADADVEALRRLSDNLAAAFR---SPED 50
 Db 15 afsdsdisngssiccvatttttttaaaenslsfpaadaallrlsenidslfqpslsld 74
 QY 51 FAFLADARIAVPGGGGGDLRVHRCVLSARSPPFLRGVFARRAAAGGGGGDSER--- 107
 Db 75 sdsfadakivv---sgdsrevavhrcvlsrsffirsafaskreke-----erdkervvk 127
 QY 108 LELRELLGGGEEVEVGYEALRLVDLYSGRVGDLPRACLCVDEDCAHVCHPAVAFM 167
 Db 128 lelkdlag-----dfevgfdsvvavigyysgkvrnlprgicvcdedsheacrpaivdv 183
 QY 168 AQVFAASTFQVAELTNLFQRRLDLVDKVEVDNLLILSVANLKNCKMKLIERCLDMV 227
 Db 184 vevlyshkfeivevlsyqrhlldiklpadvvlsvaemcgnacdgllaridki 243
 QY 228 VRSNLDMTLEKSLPPDVVKIIDARLSGLISPENKGFNPKHVRIHRLDSDDELVELVR 287
 Db 244 vrsldvttidkslpqnvkvqldtrkelgfttegrvefepdkhvkrihraldsddvelvr 303
 QY 288 MLTETQNLDDAFALHVAHEHCHSKITTELDDALADVNHRNPRGYTVLHIAARRREPK 347
 Db 304 mlkerhttdiddayahyahchdaktttellelgadvnlrnlrghtvvhvaamrkepk 363
 QY 348 IIVSLLTGKARPADVTDFGKRAVQISKRLTKQGYFGVTEEGKSPKDRLCIEILEQAER 407
 Db 364 iivslitkgahpsditsddkalkakrltkavdyfktteggkdpakdrclcieleqaer 423
 QY 408 RDPQLGEASVSLMAGESLRGLLYLENRVALARIMPFMEARVAMDAQVDTLEFNLGS 467
 Db 424 repllgegsvsakagddlrmlklylenrvalarilfpmeakvamdiaqvdgtseftlsk 483
 QY 468 GANPPPERQRTVVDLNEPFIKKEEHLARMTALSKTVELGKRFPPRCNSVLDTM--DE 525
 Db 484 nl---adarrnavdineapflkkehlgmkalsktvelgrffprcsdvlnkmdaei 540
 QY 526 TDPVSLGRDTSAE---KKRPHDLQDVLOKAFHEDKEENDRSLSSSSSTSGAIRP 580
 Db 541 sqlafigkdpcegrkrkryielqldalkteedkeefdrstlssssstpmg--rp 596

RESULT 7
 AAG17533
 ID AAG17533 standard; Protein; 593 AA.
 XX
 AC AAG17533;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 18588.
 XX
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

[illegible]

PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 43.5%; Score 1285; DB 21; Length 593;
 Best Local Similarity 47.3%; Pred. No. 1.8e-115;
 Matches 274; Conservative 113; Mismatches 164; Indels 28; Gaps 9;

QY 5 TSHVTNAFSDSDSASVEEGDADADAEALRLSDNLAARFSPEDFAFLADARIAVPGG 64
 DB 17 tsfvtatndtssivlaaeqvtgpdvsalqlslmsfesvfdspdd--fysdaklvi--- 71
 QY 65 GGGGDLRVHRCVLSARSFPLRGVFAARRAAAGGCGEDGSEKLEIRELLGGGGEVEVG 124
 DB 72 -sdgrvsthrvlsarsffksala--aakkekdsnttaavkkllel---akdyevg 124
 QY 125 YEALRLVLDYLSGRVGLPKAACLCVDECAHVGHCPAPAFMAQVLFASSTFOVAELTN 184
 DB 125 fdsvtvlayysrvppkgvsecadcnchvacrpavdflmlevlylafripelvt 184
 QY 185 LFQRRLLDVKVEVDNLLILSVANLCNCKMKLERCLDMVRSNLDMLTEKSLPPD 244
 DB 185 lyqrhlldvkviedtiylkianicgkacmkllldrckelivksnvdmsvlskslpee 244
 QY 245 VIKQIIDARLSGLISFENKPNKVRHRLALSDSDVVELVPMLLTEGQTNLDDAFALH 304
 DB 245 lvkeiidrrkleglvpkvk---khvsnvhkaldsddielvklldkhtnlddcaalh 300
 QY 305 YAVEHCDSKTTTLLDLALADVNRHPRGTYVLHIAARREPKIIVSLTKGARPADVTF 364
 DB 301 favaycnvktatdlldladvnhrrprgtyvlhvaamrkeppllislekgasaseatl 360
 QY 365 DGRKAVQISKRITKOGDYGVTEEGKPSPKDRILCILEQAERRDPOLGEASVSLAMAGE 424

DB 361 egrtalmiakqatmavecnnpbeqckhsikgrlcveilegedkrepiprdvppsfavaad 420
 QY 425 SLRGRLLYLENVALARIMFPMEARVAMADIAQVDGCTLEENLCSGANPPPER---QRTTV 480
 DB 421 elkmtlldlenvalaqrifpteadaamaelaemkgctcefvts---leprltgtrtsp 477
 QY 481 DLNESPFIKKEHLARMTALSKTVELGKRRFFPRCSNVLDKIMD-DETDPSVSLGRDTSAR 539
 DB 478 gvkiapfrileehqsrkalsktvelgkfrfrcsavlqimncedltqlacgeddtaek 537
 QY 540 R---KRFHDLQVLOKAFHEKENDRSGLSSSSSTS 574
 DB 538 riqkqymeiqetlikafsednlelgnssltstdsts 576

RESULT 8
 AAW64435
 ID AAW64435 standard; Protein; 593 AA.
 XX
 AC AAW64435;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE A. thaliana NIM-1 protein.
 XX
 DE NIM-1; noninducible immunity; systemic acquired resistance; SAR;
 KW pathogen; disease; protection; immunomodulated; plant; cereal; fruit;
 KW vegetable; virus; fungi; bacteria; insect; nematode; microbicide.
 XX
 OS Arabidopsis thaliana.
 XX
 PN WO9829537-A2.
 XX
 PD 09-JUL-1998.
 XX
 PF 23-DEC-1997; 97WO-EP07253.
 XX
 PR 10-JAN-1997; 97US-0035024.
 PR 27-DEC-1996; 96US-0034378.
 XX
 PA (NOVS) NOVARTIS AG.
 XX
 PI Friedrich LB, Molina Fernandez A, Ryals JA, Uknes SJ;
 DR WPI: 1998-388119/33.
 DR N-PSDB; AAV45273.
 XX
 PT Protection of immunomodulated plants against pathogens - comprises
 XX applying microbicide to provide increase in resistance
 PS Claim 6; Page 103-106; 164pp; English.

CC This sequence represents the NIM-1 protein from Arabidopsis thaliana.
 CC This protein is used in a method resulting in the protection of an
 CC immunomodulated plant having a first level of resistance and involves
 CC treatment with at least 1 microbicide that confers a second level of
 CC resistance, such that the plants have a third level of resistance greater
 CC than the sum of the first two levels. The method can be applied to a wide
 CC variety of plants (cereals, fruits, oilseeds, vegetables etc.) to protect
 CC against viruses, fungi, bacteria, insects and nematodes. The method
 CC provides a high level of resistance and allows a reduction in the amount
 CC of microbicide used. Since the process involves two different methods of
 CC protection, it is unlikely that the pathogen will develop resistance to
 CC the treatment.

XX Sequence 593 AA;

Query Match 43.2%; Score 1276; DB 19; Length 593;
 Best Local Similarity 47.2%; Pred. No. 1.3e-114;
 Matches 273; Conservative 113; Mismatches 165; Indels 28; Gaps 9;
 QY 5 TSHVTNAFSDSDSASVEEGDADADAEALRLSDNLAARFSPEDFAFLADARIAVPGG 64

```

Db 17 tsfvtatntdssivylaaevltgpdvsalqlsnsfsvfddpdd--fysdaklvi--- 71
Qy 65 GGGGDLRVHRCVLSARSFPLRGVFARRAAAAAGGGGDSERLELRELLGGGEEVEVG 124
Db 72 -sdgrevsfhrvlsarsfsfksala--aakkeksnntaavklelkei---akdyevg 124
Qy 125 YEALRLVDLYSGRVGDLPKAACLCVDECAHVCHGHPAVAFMAQVLFPAASTFOVAELTN 184
Db 125 fdsvtvlayvyssrvpppgvsecadencchvacrpavdvmlevlylafikipeelit 184
Qy 185 LFQRRLLDVLKVEVDNLLILSVANLCKNSCKMLLERCCLDMVVRSLNLDITLTKSLPPD 244
Db 185 lyqrhlldvdkviedtlvilkancgkacmklldrckeilvksnvmvslksipee 244
Qy 245 VIKQIIDARLSGLITSPENKGFPHKVRRIHRAALDSDDELVRMLLTGEGTNLDDAFALH 304
Db 245 lvkeidrrkelglevpkvk---khvsnvhkaldsddielvklkedhtnldacalh 300
Qy 305 YAVEHCDSKITTELLDLALADVNRHNPGRGYTVLHIAARRREPKEIIVSLTLKGPADVTF 364
Db 301 favaycnvktatdlkldadvnrhnpgrgytvhlhvaamrkepqilsllekgasaseatl 360
Qy 365 DGRKAVQISKRLTKQGYFGVTEGKSPKDRLCIEILEQARRDPOLGCEASVSLAMAGE 424
Db 361 egrtalmiakqatnavecnnpieqckhslkgrlcvlelleqgedkreqiprdvppsfaavaad 420
Qy 425 SLRGRLLYLENRVALARIMFPMPEARVAMDIQVDTGLEFNLGSGANPPPER---QRTTV 480
Db 421 elkmtdlenrvalaqlrfpteagaameiaemkgtecfivts---lepdrltgkrtsp 477
Qy 481 DLNESPFIMKEEHLARMTALSKTVELGKRFPGRCSNVLDKTMD-DETPVSLGRDTSAEK 539
Db 478 gvkiapfrileehqsrkalsktvelgkrffrcsavidqimncedltqlacgeddtaek 537
Qy 540 R-----KRPFDLQDVLOKAFHEDKEENDRSGLSSSSSSSTS 574
Db 538 rlgkqkrymeiqetlkkafsednlelgnssltatssts 576

RESULT 9
AAW46940
ID AAW46940 standard; Protein; 593 AA.
AC AAW46940;
XX
XX
XX
XX 17-AUG-1998 (first entry)
XX Arabidopsis thaliana acquired resistance protein.
KW NPRI gene; acquired resistance; disease; plant pathogens; bacteria;
KW mycoplasma; fungi; insects; nematodes; viruses; viroids;
KW transgenic.
XX
XX Arabidopsis thaliana.
XX Key Location/Qualifiers
XX Region 252..265
XX FT /note= "potential nuclear localisation signal"
XX Region 541..554
XX FT /note= "potential nuclear localisation signal"
XX
XX W09806748-A1.
XX
XX 19-FEB-1998.
XX
XX 08-AUG-1997; 97WO-US13994.
XX
XX 16-MAY-1997; 97US-0046769.
XX 09-AUG-1996; 96US-0023851.
XX 10-JAN-1997; 97US-0035166;
XX
XX (GEMO ) GEN HOSPITAL CORP.

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PA (UYDD-) UNIV DUKE.
PI Ausubel FM, Cao H, Dong X, Glazebrook J;
XX
XX WPI: 1998-159458/14.
XX N-PSDB; AAV16851.
XX
XX New isolated plant acquired resistance polypeptide gene - useful
XX for, e.g. producing plants with increased resistance to pathogens
XX such as bacteria
XX
XX Claim 26; Fig 5; 127pp; English.
XX
XX The sequence is that encoded by the acquired resistance gene
XX NPRI. It may be produced by transgenic cells which are useful
XX in the production of plants having an increased level
XX of resistance against disease caused by plant pathogens, e.g.
XX bacteria, mycoplasmas, fungi, insects, nematodes, viruses,
XX and viroids.
XX
XX Sequence 593 AA;

Query Match 43.2%; Score 1276; DB 19; Length 593;
Best Local Similarity 47.2%; Pred. No. 1.3e-114;
Matches 273; Conservative 113; Mismatches 165; Indels 28; Gaps 9;

Qy 5 TSHVTNFAFSDSDSASVEEGDADADADVDEALRRLSDNLAAAFRSPEDFAFLADARIAPGG 64
Db 17 tsfvtatntdssivylaaevltgpdvsalqlsnsfsvfddpdd--fysdaklvi--- 71
Qy 65 GGGGDLRVHRCVLSARSFPLRGVFARRAAAAAGGGGDSERLELRELLGGGEEVEVG 124
Db 72 -sdgrevsfhrvlsarsfsfksala--aakkeksnntaavklelkei---akdyevg 124
Qy 125 YEALRLVDLYSGRVGDLPKAACLCVDECAHVCHGHPAVAFMAQVLFPAASTFOVAELTN 184
Db 125 fdsvtvlayvyssrvpppgvsecadencchvacrpavdvmlevlylafikipeelit 184
Qy 185 LFQRRLLDVLKVEVDNLLILSVANLCKNSCKMLLERCCLDMVVRSLNLDITLTKSLPPD 244
Db 185 lyqrhlldvdkviedtlvilkancgkacmklldrckeilvksnvmvslksipee 244
Qy 245 VIKQIIDARLSGLITSPENKGFPHKVRRIHRAALDSDDELVRMLLTGEGTNLDDAFALH 304
Db 245 lvkeidrrkelglevpkvk---khvsnvhkaldsddielvklkedhtnldacalh 300
Qy 305 YAVEHCDSKITTELLDLALADVNRHNPGRGYTVLHIAARRREPKEIIVSLTLKGPADVTF 364
Db 301 favaycnvktatdlkldadvnrhnpgrgytvhlhvaamrkepqilsllekgasaseatl 360
Qy 365 DGRKAVQISKRLTKQGYFGVTEGKSPKDRLCIEILEQARRDPOLGCEASVSLAMAGE 424
Db 361 egrtalmiakqatnavecnnpieqckhslkgrlcvlelleqgedkreqiprdvppsfaavaad 420
Qy 425 SLRGRLLYLENRVALARIMFPMPEARVAMDIQVDTGLEFNLGSGANPPPER---QRTTV 480
Db 421 elkmtdlenrvalaqlrfpteagaameiaemkgtecfivts---lepdrltgkrtsp 477
Qy 481 DLNESPFIMKEEHLARMTALSKTVELGKRFPGRCSNVLDKTMD-DETPVSLGRDTSAEK 539
Db 478 gvkiapfrileehqsrkalsktvelgkrffrcsavidqimncedltqlacgeddtaek 537
Qy 540 R-----KRPFDLQDVLOKAFHEDKEENDRSGLSSSSSSSTS 574
Db 538 rlgkqkrymeiqetlkkafsednlelgnssltatssts 576

RESULT 10
AAW23963
ID AAW23963 standard; Protein; 593 AA.
XX
XX AAW23963;

```


XX DT 17-JUN-1998 (first entry)

XX DE Arabidopsis thaliana NIM1 protein.

XX KW NIM1; noninducible immunity; disease resistance; plants;

XX KW SAR gene expression.

XX OS Arabidopsis thaliana.

XX PN WO9749822-AL.

XX PD 31-DEC-1997.

XX PF 10-MAR-1997; 97WO-EP01218.

XX PR 10-JAN-1997; 97US-0035022.

XX PR 21-JUN-1996; 96US-0020272.

XX PR 30-AUG-1996; 96US-0024883.

XX PR 13-DEC-1996; 96US-0033177.

XX PR 27-DEC-1996; 96US-0773559.

XX PA (NOVS) NOVARTIS AG.

XX PI Delaney TP, Ellis DM, Friedrich LB, Johnson JE;

XX PI Lawton KA, Ryals JA, Weymann K;

XX DR WPI; 1998-077185/07.

XX DR N-PSDB; AAV04632.

XX NIM1 gene which allows activation in plant of systemic acquired

PT resistance - useful to confer broad spectrum disease resistance in

PT plants, specifically crop plants, e.g. rice, wheat, barley, rye and

PT corn

XX Disclosure; Fig 15; 153pp; English.

XX The sequence is that of the NIM1 (noninducible immunity) protein. It

CC may be used to confer a broad spectrum disease resistance in plants,

CC specifically crop plants, e.g. rice, wheat, barley, rye and corn.

CC The NIM1 gene can be used to confer universal disease susceptibility

CC to plant cells, and their progeny. It can also be used in a screening

CC method for identifying compounds capable of inducing broad spectrum

CC disease resistance in plants, while the plant cells, and their

CC progeny, can be used to isolate a gene fragment which allows

CC expression of broad spectrum disease resistance in plants, or to

CC incorporate the resistant trait into plant lines through breeding.

XX SQ Sequence 593 AA;

Query Match 43.2%; Score 1276; DB 19; Length 593;

Best Local Similarity 47.2%; Pred. No. 1.3e-114;

Matches 273; Conservative 113; Mismatches 165; Indels 28; Gaps 9;

QY 5 TSHVTNAFSDSASVEEGDADADADVEALRLSDNLAARSPDEAFADARIAVPGG 64

DB 17 tsfvatndtssivylaaeqvltgpdvsalqlnsfsvfddpdd--fysdskivi--- 71

QY 65 GGGGDLRHVRCLVSARSFPLRGVFARRAAAGGGGDSERLELRELLGGGEEVEYG 124

DB 72 -sdgrevsfhrvcvlsarsffksala--aakkeksnntaavkkllel---akdyevg 124

QY 125 YEALRLVLDYLSGRVGDLPKACLCVDECAHVGHCHPAVAFMAQVLPFAASTFOVAELTN 184

DB 125 fdsavtvlayvysrrvpkpgvsecadncchvacrpavdmflevlylafikfpelit 184

QY 185 LFQRELLDVLKVEVDNLLILSVANLCKMCKMLERCLDMVVRNSNLDMLTEKSLPDD 244

DB 185 lqrhldvkvviedtivilkianicgacmkllorckelivsvndmvsleksipee 244

QY 245 VIKQITDARLSLGLISPENKGFNKHVRRIHRAALDSDDDVELVRMLLTGQTNLDDAFALH 304

DB 245 lvkeiidrrkelglevpkvk---khvsnvhkaldsddielvklilkedhtnlddcalh 300

QY 305 YAVEHCDSKITTELLDLALADVNHNRNPRGYTVLHIAARRREPKIIVSLTKGARPADVTF 364

DB 301 favaycnvxtatdlkladlvnhrnprgytvlhvaamrkepqllilsllekgsaseatl 360

QY 365 DGRKAVOISKRLTKQGYFEGVTEEGKPSKDRCLICILBOAERRDPOLGEASVSLAMAGE 424

DB 361 egrtalmiakqatmavecnipeqkshkgrlclvlelqeqdreqiprdvppsfaaad 420

QY 425 SLRGLLYLENVALARIMFPMPEARVAMDIAQVDGTFLEFNLGSGANPPPER----QRTTV 480

DB 421 eikmtlldlenvalaqrifpteaaqameiaemkgctcefvts---lepdrllgtkrtsp 477

QY 481 DLNESPFINKEEHLARMTALSKTVELGKFRFPKCSNVLDKIMD-DETDVPSLGRDTSARK 539

DB 478 gvkiapfrileehqsrklasktvelgkfrfpcrsavldqimncedltqlaceddtaek 537

QY 540 R----KRPHDLQDLVQKAFHEKDEKENDRSGLSSSSSSTS 574

DB 538 riqkkqymeiqetlkkafsednlelgnssldststs 576

RESULT 11

AAW61982

ID AAW61982 standard; Protein; 593 AA.

XX AC AAW61982;

XX DT 29-SEP-1998 (first entry)

XX DE A. thaliana non-inducible immunity-1 (NIM1) wild-type protein.

XX KW Non-inducible immunity-1 gene; NIM1 gene; disease resistance; mutant;

XX KW transgenic plant; SAR; systemic acquired resistance; CIM; pathogen;

XX KW constitutive immunity; agriculture.

XX OS Arabidopsis thaliana.

XX FH Key Location/Qualifiers

FT Misc-difference 566

FT /label= Ser, Ala

FT /note= "indicated differently in different parts of

FT the specification"

XX PN WO9826082-AL.

XX PD 18-JUN-1998.

XX PF 12-DEC-1997; 97WO-EP07012.

XX PR 20-JUN-1997; 97US-0880179.

XX PR 13-DEC-1996; 96US-0033177.

XX PR 27-DEC-1996; 96US-0034379.

XX PR 27-DEC-1996; 96US-0034382.

XX PR 10-JAN-1997; 97US-0034730.

XX PR 10-JAN-1997; 97US-0035021.

XX PR 10-JAN-1997; 97US-0035022.

XX PA (NOVS) NOVARTIS AG.

XX PI Friedrich LB, Hunt MD, Lawton KA, Ryals JA, Steiner HW;

XX PI Uknes SJ;

XX DR WPI; 1998-348536/30.

XX DR N-PSDB; AAV43659.

XX use of non-inducible immunity-1 gene - for transforming plants to

PT produce transgenic plants having a broad spectrum disease resistance

XX Example 15; Pages 108-116; 205pp; English.

XX This represents the Arabidopsis thaliana non-inducible immunity-1 (NIM1)

CC wild-type protein. This can be mutated to produce altered forms of
 CC the NIM1 protein. The invention provides a chimeric gene comprising a
 CC promoter active in plants operatively linked to a DNA molecule that
 CC encodes an altered form of the NIM1 protein. Plant cells stably
 CC transformed with a recombinant vector comprising such a chimeric gene
 CC have a broad spectrum of disease resistance. The altered NIM1 proteins
 CC act as dominant-negative regulators of the systemic acquired resistance
 CC (SAR) signal transduction pathway. The transgenic plants transformed with
 CC an altered NIM1 gene exhibits constitutive SAR expression which is higher
 CC in the transformed plants than in a wild-type plant. The products can be
 CC used for producing plants with a broad spectrum disease resistance.
 CC Overexpression of NIM1 mimics the effects of inducer compounds that
 CC induce constitutive immunity (CIM) phenotype in plants. The inventions
 CC can be used with plants such as rice, wheat, barley, rye, corn, potato,
 CC carrot, sweet potato, sugar beet, bean, pea, chickory, lettuce, cabbage,
 CC cauliflower, broccoli, turnip, radish, spinach, asparagus, onion, garlic,
 CC eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber,
 CC apple, pear, quince, melon, plum, cherry, peach, nectarine, apricot,
 CC strawberry, grape, raspberry, blackberry, pineapple, avocado, papaya,
 CC mango, banana, soybean, tobacco, tomato, sorghum and sugarcane. The
 CC plants produced are resistant to plant pathogens such as viruses,
 CC viroids, fungi, bacteria, insects such as aphids and lepidoptera and
 CC nematodes. The plants produced can be used in agriculture.
 XX
 XX Sequence 593 AA;

Query Match 43.1%; Score 1272; DB 19; Length 593;
 Best Local Similarity 47.0%; Pred. No. 3.2e-114;
 Matches 272; Conservative 113; Mismatches 166; Indels 28; Gaps 9;

Qy 5 TSHVTNAPSDDSDASVEGDADADADVEALRLSDNLAAAFSPEDFAFLADARIAVPGG 64
 Db 17 tsfvtatndtsiivylaaevltpdvlsalqlnsfsvfddpd--fysdakivl--- 71
 Qy 65 GGGGDLRVHRCVLSARSPFLRGVFARRAAAAGGGGDSERLELRELLGGGEEVEVG 124
 Db 72 -sdgrevsfhrvcvlsarsffksala--aakkeksnntaavkielkei---akdyevg 124
 Qy 125 YEALRLVLDYLSRGVGLDPRACLCVDEDCAHVGCHPAVAFMAQVLPFAAFTFOVALTN 184
 Db 125 fssvvtviavyyssrvrppkvgsecadcnchvacrpavdmlevlylafikipelit 184
 Qy 185 LFORLLDLVDKVEVDNLLTSLVANLCKCMKLLERCLDMVVRSLDMLTLEKSLPPD 244
 Db 185 lqyrhlavdkviedtlvilkianicgkcmkldrcckeiivksnvdmsleksipee 244
 Qy 245 VIKQIIDARLSGLISPENKGPNNKHVRIHRLDSDVDELVRLMLLTGQTNLDDAFALH 304
 Db 245 lvkeidrrkelglevpkvk---khvsnvhkaidssddielvklkldednlddacaalh 300
 Qy 305 YAVEHCDISKITELDLALADVNHNPRGYTVLHTAARREPKIIVSLITKGPADVTF 364
 Db 301 favaycnvktatdlklldadnhrnprgytvlvhaamrkepqilslilekgasaseatl 360
 Qy 365 DGRKAVQISKRLTKGDFYGVTEGKPSKDRCLCTEILEQAERPPQDGEASVSLAMAGE 424
 Db 361 egrtalmiakqatmavecnnpieqckshlkgvlveileqedkreqiprdvppsfavaad 420
 Qy 425 SLRGRLLYLENVALARIMFPEARVAMDIQAVDGTLEFNLGSGANPPPER---QRTTV 480
 Db 421 elkmtdlidenvalaqlrfpteaaameiaemkgctcefvts---lepdrltgtkrtsp 477
 Qy 481 DLNESPFFIMKEHLARMTALSKTVELGRFFPRCSNVLDKIMD-DETPVSLGRDTSAEK 539
 Db 478 gvklaipfrileehqgrlkaletkveigkrffprcsavldqimmoedltqlacgeddtaek 537
 Qy 540 R----KRFHDLDVQLQAFHEDKENDRSGLSSSSSSTS 574
 Db 538 rlqkqrymeiqetlkkafsednlelgnxsltdtssts 576

RESULT 12

AAW64436
 ID AAW64436 standard; Protein; 593 AA.
 XX
 AC AAW64436;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE A. thaliana variant NIM-1 protein #1.
 XX
 KW NIM-1; noninducible immunity; systemic acquired resistance; SAR;
 KW pathogen; disease; protection; immunomodulated; plant; cereal; fruit;
 KW vegetable; virus; fungi; bacteria; insect; nematode; microbicide.
 XX
 OS Arabidopsis thaliana.
 XX
 XX Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 55 /label= S55A
 FT /note= "Wild-type Ser is replaced by Ala"
 FT Misc-difference 59 /label= S59A
 FT /note= "Wild-type Ser is replaced by Ala"
 FT
 XX WO9829537-A2.
 XX
 XX 09-JUL-1998.
 XX
 XX 23-DEC-1997; 97WO-EP07253.
 XX
 XX 10-JAN-1997; 97US-0035024.
 XX
 XX 27-DEC-1996; 96US-0034378.
 XX
 XX (NOVS) NOVARTIS AG.
 XX
 XX Friedrich LB, Molina Fernandez A, Ryals JA, Uknes SJ;
 XX WPI: 1998-388119/33.
 XX N-PSDB; AAV46275.
 XX
 XX Protection of immunomodulated plants against pathogens - comprises
 XX applying microbicide to provide increase in resistance
 XX
 XX Claim 10; Page 120-123; 164pp; English.
 XX
 XX This sequence represents a variant NIM-1 protein from Arabidopsis
 XX thaliana. This protein is used in a method resulting in the protection of
 XX an immunomodulated plant having a first level of resistance and involves
 XX treatment with at least 1 microbicide that confers a second level of
 XX resistance, such that the plants have a third level of resistance greater
 XX than the sum of the first two levels. The method can be applied to a wide
 XX variety of plants (cereals, fruits, oilseeds, vegetables etc.) to protect
 XX against viruses, fungi, bacteria, insects and nematodes. The method
 XX provides a high level of resistance and allows a reduction in the amount
 XX of microbicide used. Since the process involves two different methods of
 XX protection, it is unlikely that the pathogen will develop resistance to
 XX the treatment.
 XX
 XX Sequence 593 AA;

Query Match 43.0%; Score 1270; DB 19; Length 593;
 Best Local Similarity 47.0%; Pred. No. 5e-114;
 Matches 272; Conservative 113; Mismatches 166; Indels 28; Gaps 9;

Qy 5 TSHVTNAPSDDSDASVEGDADADADVEALRLSDNLAAAFSPEDFAFLADARIAVPGG 64
 Db 17 tsfvtatndtsiivylaaevltpdvlsalqlnsfsvfddpd--fysdakivl--- 71
 Qy 65 GGGGDLRVHRCVLSARSPFLRGVFARRAAAAGGGGDSERLELRELLGGGEEVEVG 124
 Db 72 -sdgrevsfhrvcvlsarsffksala--aakkeksnntaavkielkei---akdyevg 124

QY 425 SLRGLLYLENVALARIMFPMARVAMIAQVDGTLFNLGSGANPPPER---QRTTV 480
 Db 421 elktlidlennvalaqlrftpeaaameiaemkgtcefiivs---lepdrllgtkrtsp 477
 QY 481 DLNESPIMKEEHARMTALSKTVELKRPFRPCSNVLDKIMD-DETDPSVSLGRDTSAEK 539
 Db 478 gvkiapfriieehqsrkalsktvelgrfprcsavldqimnceditqlacgeddtaek 537
 QY 540 R---KRFHDLQVLOKAFHEDKEENDRSGLSSSSSSSTS 574
 Db 538 rlqtkgrymeiqetikkafednlelgnlsitdststs 576

RESULT 14

AA27303
 ID AAB27303 standard; Protein: 579 AA.

AC AAB27303;

DT 25-JAN-2001 (first entry)

XX B. napus NIM1 homologue SEQ ID NO: 6.

DE Systemic acquired resistance; SAR; signal transduction cascade;
 KW disease resistance; tobacco; tomato; canola; sunflower; sugarbeet;
 KW potato.

OS Brassica napus.

XX WO200053762-A2.

PN 14-SEP-2000.

XX 07-MAR-2000; 2000WO-EP01978.

XX 09-MAR-1999; 99US-0265149.

XX (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX Salmeron JM, Weisio LJ, Willits MG, Mengiste T;

XX WPI; 2000-594322/56.

DR N-PSDB; AAA97192.

PT Novel plant genes for enhancing systemic acquired resistance gene
 PT expression and broad spectrum disease resistance in plants, are
 PT homologues of Arabidopsis NIM1 gene -

XX Claim 1; Page 80-81; 152pp; English.

XX The present invention is concerned with the isolation of NIM1 homologues
 CC and their coding sequences from Arabidopsis thaliana, Brassica napus,
 CC Nicotiana tabacum, Lycopersicon esculentum, Beta vulgaris, Helianthus
 CC annuus and Solanum tuberosum. NIM1 is one of the proteins involved in the
 CC signal transduction cascade leading to systemic acquired resistance (SAR)
 CC in plants. This gives the plants an increased resistance to disease. The
 CC protein and gene can be used to produce transgenic plants resistant to
 CC diseases caused by viruses, such as tobacco or cucumber mosaic virus,
 CC ringspot virus, perlongium leaf curl virus, red clover mottle virus,
 CC tomato bushy stunt virus, fungi, including Phytophthora parasitica and
 CC Peronospora tabacina, bacteria such as Pseudomonas syringae and P.
 CC tabaci, insects, including aphids and lepidoptera and nematodes such as
 CC Meloidogyne incognita. In particular they can be used against disease
 CC organisms of maize.

XX Sequence 579 AA;

Query Match 41.4%; Score 1222.5; DB 21; Length 579;
 Best Local Similarity 45.9%; Pred. No. 1.9e-109;
 Matches 260; Conservative 110; Mismatches 160; Indels 37; Gaps 10;

QY 14 DSDSASVEEGDADADADVEALRRLSDNLAAAFSPEDFAFLADARIAVPGGGGGDLRV 73
 Db 27 nsgstvxptelxtrpvsafllslesvfdspe--afysdaklavl----sddkevsf 80
 QY 74 HRCVLSARSFPLRGVFPARRAAAAGGGGCGSERLELRELLGGGGEVEGYEALRLVLD 133
 Db 81 hrcillsars-----lffkaalxaaekvqskpvtklektl----aaeydvfgdsvavla 131
 QY 134 YLXSGRVGDLPKAACLCVDECAHVGCHPAVAFMAOVLFFAASTFOVAELNLFQRLLDV 193
 Db 132 yvysgrvrpppkgysecadxschvacrpavdmvevilylafvfqgelvtmgyrhlldv 191
 QY 194 LDKVEVDNLLILSVANLCKNCKMLERCLDMVVRNLDMLTLEKSLPPDVIKQIIDAR 253
 Db 192 vdkvxiedtlvklanicgackkifdkcreiivksnvdvtlkkslpexiakqvidir 251
 QY 254 LSLGLISPENKGFPHVRIHRALSDDDVELVRLMLTEGOTNLDLDAFALHYAVEHCDSK 313
 Db 252 keiglevae---pekhsvsnihkalesddldlvmllikeghtnldeayalhfvaycdek 307
 QY 314 ITTELDDLALADVNHNRPRGTYVLHIAARRRPEKIIIVSLTLTGARPADVTFDGRKAVQIS 373
 Db 308 tarnliegfadvnrnrprgtyvihuamrkeptliallittkganalemsldgrtallia 367
 QY 374 KRUTKQDYEGVTEEGKPSKRLCIEILQABER-RDPQLGEASVSLAMAGESLGRLLY 432
 Db 368 kvtkaaec--ilekgklaakgvcveilkpndntrepfedvpslvaadqfkrild 426
 QY 433 LENRVALARIMFPMARVAMIAQVDGTLFNLGSGANPPPERQRTTVLDNESPIMKEE 492
 Db 427 lenrvqmarclypmeaqvamdfarmkgtrefv-----ttatdlhmeprfkfvm 475
 QY 493 HLAARMTALSKTVELKRPFRPCSNVLDKIMDDE--TDPVSLGRDT---SAEKRRRPHDLQ 547
 Db 476 hqsriltalsktvfgkrffprcskvladiivdsedtlilaiveedtpqgrgkrqrfmeiq 535
 QY 548 DVLOKAFHEDKEENDRSGLSSSSSSSTS 574
 Db 536 eivqmafskdkedlgskslsassts 562

RESULT 15

AA27307
 ID AAB27307 standard; Protein: 600 AA.

XX AAB27307;

XX 25-JAN-2001 (first entry)

XX A. thaliana NIM1 homologue SEQ ID NO: 20.

XX Systemic acquired resistance; SAR; signal transduction cascade;
 KW disease resistance; tobacco; tomato; canola; sunflower; sugarbeet;
 KW potato.

XX Arabidopsis thaliana.

XX WO200053762-A2.

PD 14-SEP-2000.

XX 07-MAR-2000; 2000WO-EP01978.

XX 09-MAR-1999; 99US-0265149.

XX (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX Salmeron JM, Weisio LJ, Willits MG, Mengiste T;

XX WPI; 2000-594322/56.

XX N-PSDB; AAA97202.

Search completed: July 12, 2001, 17:13:31
Job time: 53 sec

PT Novel plant genes for enhancing systemic acquired resistance gene
PT expression and broad spectrum disease resistance in plants, are
PT homologues of Arabidopsis NIM1 gene -

PS Claim 1; Page 98-100; 152pp; English.

The present invention is concerned with the isolation of NIM1 homologues and their coding sequences from *Arabidopsis thaliana*, *Brassica napus*, *Nicotiana tabacum*, *Lycopersicon esculentum*, *Beta vulgaris*, *Helianthus annuus* and *Solanum tuberosum*. NIM1 is one of the proteins involved in the signal transduction cascade leading to systemic acquired resistance (SAR) in plants. This gives the plants an increased resistance to disease. The protein and gene can be used to produce transgenic plants resistant to diseases caused by viruses, such as tobacco or cucumber mosaic virus, ringspot virus, pelargonium leaf curl virus, red clover mottle virus, tomato bushy stunt virus, fungi, including *Phytophthora parasitica* and *P. peronospora tabacina*, bacteria such as *Pseudomonas syringae* and *P. tabaci*, insects, including aphids and lepidoptera and nematodes such as *Meloidogyne incognita*. In particular they can be used against disease organisms of maize.

AA	
SQ	Sequence 600 AA;

Query Match	41.1%	Score 1213.5	DB 21	Length 600
Best Local Similarity	45.8%	Pred. No. 1.5e+108		
Matches 277	Conservative 105	Mismatches 172	Indels 51	Gaps 17
Qy	1	MEPTSHVTNFAFSDSDSASVEEGD----	ADADAD-----	VEALRRRLSDNLAAAFR 46
Db	1			
Qy	47	SPEDFAFLADARIAPVGGGGGDLRHVRCVLSRASPRLGRVFARRAAAAAGGGGDEGSE 106		
Db	61	spe--tfysdaklvl---aggrevsfrcilsarip----	vfksalatvkeqtsstiv 109	
Qy	107	RLEURELLGGGGEVEVGYEARLVLDLYLSGRGVLDLPKAACLCVDEDCAHVGHCHPAVAF 166		
Db	110	klqlkei-----ardveygfdsvavlayvyysgrvrsppkgsacvdddcchvacrskvdf 165		
Qy	167	MAQVLFRAASTFOVAELTNLFORRLLDVLDKVEVDNLLLLILSVANLCNKSKMLLERCLDM 226		
Db	166	mvevlyisfvfqlgelvtlyerqflevtkvkvvedilvifkldtlcgtttkldirciei 225		
Qy	227	VVRSLNDIMITLKSIPDPDVIKQIIDARLSGLISPENKGFNKHVRRTHRALDSDDVLEV 286		
Db	226	ivksdielvsleksipqhfqioldrfeleppkle----	rivnklykaldsdvdelv 281	
Qy	287	RMLLATEGOTNLDDAFALHYAVEHCDSKTTITELLDLADVNHRNPRGVTVLHIAARREP 346		
Db	282	kmllilegthnldeayalhfaheacvktaydlleleladvnlrnpgrtyvlhvaamrkep 341		
Qy	347	KTIIVSLTKGARPADVTDFGRKAVOISKRLLTKQGDYFGVTEEGRSPSKDRLCIELEQAE 406		
Db	342	kliisllmkganildtldgrtalvivkrllckaddyktstedgtpsllkggicievleh-e 400		
Qy	407	RRDPQLG--EASVSLMAGESLSRGLLYLENRVALARIMFMEARVAMDIQAQVDGTLEFN 464		
Db	401	qklevlspieasllpvtpeelrmllyenrvalarilfpvetetvgiaaleetceft 460		
Qy	465	LGSGANPPPE--RORTTVDLNESPFIKKEEHLARMTALSKTVELGKRFPPCRSNVLDKIM 522		
Db	461	-asslepdhhlgelrtdsldumafqihelksrlraicckveigkyfkrccs--ldhfm 517		
Qy	523	DDE--TDPVSLGRDT---SAEKRFRHFDQDLQAFKHEEDRSGLESSSSSSSTIGA 577		
Db	518	dtedlnhlasveedtpkrlqkkrymelgetlmlktfsedkee---cgkstptpts--a 572		
Qy	578	IRPRR 582		
Db	573	visnr 577		

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OM nucleic - nucleic search, using sw model

Run on: July 11, 2001, 07:14:42 ; Search time 1544.62 Seconds
(without alignments)
12484.508 Million cell updates/sec

Title: US-09-294-539-3

Perfect score: 2040

Sequence: 1 atggagccgcgcagcagcca.....caaaaaaaaaaaaaaaaaa 2040

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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EST:*

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2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
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202: em_gss_hum9:*
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204: em_gss_inv2:*
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251: gb_gss34:*
252: em_gss_inv4:*
253: em_gss_rodl6:*
254: em_gss_rodl7:*
255: em_gss_rodl8:*
256: gb_gss35:*
257: gb_gss36:*
258: gb_gss37:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	442.2	21.7	614	154	BG464249	EM1_71_D1
2	352.6	17.3	455	136	BE493178	WHE0570_C
3	213.6	10.5	666	154	BG464574	EM1_71_D1
4	208.6	10.2	573	31	AV551266	AV551266
5	204.2	10.0	613	112	AW160235	EST290093
6	181.4	8.9	450	115	AW399343	EST309843
7	160.4	7.9	667	155	BG598808	EST503708
8	158	7.7	629	256	B26306	P18D8TF IGF
9	154	7.5	458	162	BE023215	sm70a04.Y
10	152.8	7.5	654	174	BG124935	EST470581
11	149	7.3	554	115	AW352680	660034C04
12	134.6	6.6	547	141	BE918569	OVI_8_E08
13	134.6	6.6	569	120	AW715943	WS1_38_H0
14	133.2	6.5	645	114	AW310982	sg31b02.X
15	131.4	6.4	430	20	AT442277	sa66a04.Y
16	130	6.4	491	151	BF657743	OY2_17_E0
17	123.8	6.1	806	133	BG414779	HVSMEX000
18	122.2	6.0	569	166	BE366197	P11_31_F0
19	120.8	5.9	680	114	AW309867	sf25g10.X
20	120.6	5.9	562	166	BE366196	P11_31_F0
21	118.4	5.8	535	119	AW687759	NF013B05R
22	117.8	5.8	733	115	AW349633	GN210006A
23	109.4	5.4	462	105	AL372473	MCBASIC01
24	109.4	5.4	595	140	BE801977	sr23d08.Y
25	108.8	5.3	669	119	AW684122	NF012F06N
26	103.8	5.1	394	162	BE020423	sm40e08.Y
27	102.8	5.0	492	116	AW438378	707077D02
28	97.2	4.8	527	168	BF728689	1000065G0
29	96.2	4.7	516	118	AW622846	EST306916
30	95.4	4.7	670	141	BE917988	OVI_8_E08
31	95.4	4.7	736	167	BE435499	EST406577
32	94.8	4.6	556	154	BG462412	947057B04
33	92	4.5	258	188	T22612	4620_Lambda
34	92	4.5	1928	192	AK013012	Mus muscu
35	89.6	4.4	392	174	BG159609	OV2_6_G05
36	88.4	4.3	279	31	AV556619	AV556619
37	87.2	4.3	1844	170	BF856160	963057E09
38	86.4	4.2	925	219	CNS0091P	Drosophil
39	86.2	4.2	816	153	BG414781	HVSMEX000
40	85.4	4.2	935	219	CNS006XK	AL066051
41	84	4.1	925	219	CNS0091P	AL053013
42	83	4.1	335	136	BE493303	Drosophil
43	83	4.1	461	104	AI960862	sc91f07.Y
44	83	4.1	932	219	CNS0072Q	AL066742
45	82	4.0	1501	76	AW731188	GA_Ea001

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
1	BG464249	EM1_71_D12.bl_A002 Embryo 1 (EM1) Sorghum bicolor cDNA, mRNA	BG464249	EST	GI:13392562	Sorghum	Sorghum bicolor	Reid, S.P., Cordonnier-Pratt, M.-M., Gingle, A. and Pratt, L.H.	An EST database from Sorghum: developing embryos	Unpublished (2000)	
		sequence.									
		clade: Panicoideae; Andropogoneae; Sorghum.									
		1 (bases 1 to 614)									
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;									
		Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC									
		clade: Panicoideae; Andropogoneae; Sorghum.									
		1 (bases 1 to 614)									
		Reid, S.P., Cordonnier-Pratt, M.-M., Gingle, A. and Pratt, L.H.									
		An EST database from Sorghum: developing embryos									
		Unpublished (2000)									

COMMENT

Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1860
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.
Seq primer: JEN REV
High quality sequence stop: 610
POLYA=No.

FEATURES

Location/Qualifiers
1..614
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Embryo 1 (EM1)"
/note="Organ: Embryos germinated for 24 hr; Vector: pBluescript II from Lambda Zap II; Site 1: XhoI; Site 2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."
BASE COUNT 188 a 125 c 146 g 155 t
ORIGIN

Query Match 21.7%; Score 442.2; DB 154; Length 614;
Best Local Similarity 83.0%; Pred. No. 2.9e-95;
Matches 504; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 712 gagaagtcattcctccagatgttatcaagcagattatgtgacgacctaacgacctgga 771
DB 8 GAGAGGCAATGCTCCACATGTTGTCAAGCAATTTGTTGATGCAAGGCTTAAGTCTTGA 67
QY 772 ttaattccaccgaaacaaaggatttcttaacaaacatgtgaggaggtatcacagagcc 831
DB 68 TTAGTTTACCAGAGGACAAAGGCTTCCCTAACATCATGTAGAAAGAGTACACAGGCG 127
QY 832 ctgactctgacgatgtagactagctagctcactgactgacgagagacagacaaatctt 891
DB 128 CTGATTTCTGATGATGTAGAGCTAGTCCGAATGCTACTCAAGAGAGGAAATAATCTC 187
QY 892 gatgatcgttgcactgcactacgctcgaacattgtgactccaaataacacacgag 951
DB 188 GATGATGATGATGCTGATGATGATGCTGATGATGATGATGATGATGATGATGATGAT 247
QY 952 ctttggatctgcacttgcagattgatttaataatagaaacacacagaggttatactgttct 1011
DB 248 CTCTCGATCTCGCACTTGCAGATGTTAATCATAGCAACCCAAAGAGGCTATACGGTCTT 307
QY 1012 cacattgctgcaggcgaagagagcctaaataatctgtctcctcttaacacaggggct 1071
DB 308 CACATTTGCTGTATGAGAGGGAACCTAAATCATTTGCTCTCTTTTGACCAAGGAGCT 367
QY 1072 cgaccagcagatttacattcagatgggagaaagcgggtcaaatctcaaaagacacaa 1131
DB 368 CGGCCCTGAGATCTACATTTGATTCACAGAAAGAGAGTACAGATCTCTTAACAGCTTACA 427
QY 1132 aaacaaagggattacttttgggttaccgaagaagggaaaaacaccttctccaaagatggtta 1191
DB 428 AATCATGGGGATTTACTTTGGGCTTACTGAGGATGAAAGCCTTCTCTTAAGATAGATTA 487
QY 1192 tgtattgaataactgagcaagctgaaagaagggagaccccaacacacagcagagacatcagtt 1251
DB 488 TGTATTGAGATCTAGAGCAAGCTGAAAGAGGAGGCCCATCTCTTGAGAGCATCAGTT 547
QY 1252 tctcttgcattgagcaggtgaggtctcacgagaaggttgcgtatcttctgataaaacaggtt 1311
DB 548 TCTCTTGCATAGAGAGGAGACTCTGCGGCTGGAAGGTTGCTCTTACCTTGAACACCGATT 607
QY 1312 gctttgg 1318
|||||

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Db 608 GCTTAG 614

RESULT 2
LOCUS BE493178 455 bp mRNA EST 16-APR-2001
DEFINITION WHE0570_C11_F22E Triticum monococcum vegetative apex cDNA library
Triticum monococcum cDNA clone WHE0570_C11_F22, mRNA sequence.
ACCESSION BE493178
VERSION WHE0570_C11_F22
KEYWORDS Triticum monococcum
SOURCE EST.
ORGANISM Triticum monococcum.
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticaceae; Triticum.
REFERENCE 1 (bases 1 to 455)
AUTHORS Anderson,O.D., Chao,S., Dubcovsky,J., Echenique,V., Han,P.S., Hsia
,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L.,
Stamove,B. and Tong,J.C.
TITLE The structure and function of the expressed portion of the wheat
genomes - Vegetative apex cDNA library from Triticum monococcum
JOURNAL Unpublished (2001)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 510595773
Fax: 5105959818
Email: oanderson@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: StrataGene T3 primer.
FEATURES
source
Location/Qualifiers
1..455
/organism="Triticum monococcum"
/cultivar="DW92"
/db_xref="taxon:4568"
/clone="WHE0570_C11_F22"
/clone.lib="Triticum monococcum vegetative apex cDNA
library"
/tissue_type="Vegetative shoot apex"
/dev_stage="Three weeks-old plants"
/lab_host="E. coli XL0L"
/note="Vector: Lambda pBK-CMV (Lambda Zap Express),
excised phagemid; Site 1: EcoRI; Site 2: XhoI; The tissue,
total RNA, and poly(A) RNA were prepared, a cDNA library
was made, and the cDNA clones were in vivo excised at the
University of California, Davis (V. Echenique, B. Stamova
, J. Dubcovsky). Plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
other authors)."
BASE COUNT 132 a 94 c 98 g 131 t
ORIGIN
Query Match 17.3%; Score 352.6; DB 136; Length 455;
Best Local Similarity 85.9%; Pred. No. 7.6e-74;
Matches 391; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 602 acctctattgattctatgtgtgccaacttatgcaacaaatctctgcatgaactgcttg 661
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Db 1 ACCTTCCGTTGATCTATCTGTGCAAACTTATGCAACAAATCTTGCGTGAACACTGTTG 60
Qy 662 aaagatgccttgatagtgtagccggtcaaaccttgacattactcttgagaagtcac 721
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Db 61 AGAGATGCTCGAGATGGTAGTCCGGGCAAACTTGTGACATGATTACTTTGAGAAAGCAT 120
Qy 722 tgcctccagatgttatcaagcagagattattgatgcgcgcctcaagccctcgattattacac 781
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Db 121 TGCCTGAAGATGTTATCAAGCAAAATTATTGATTCAGGATAACTCTTGGATTAGCTTAC 180
Qy 782 cagaaaaacaaggagggttctcttaacaacatgtgaggaggatacacagagcccttgactctg 841

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Db 181 CCGAAGACAATGGCTGTCTCTCAACAAACACGCTAAGAAGGACTCAAGGCACCTTGATTCTG 240
Qy 842 acgatgtagagctagtcagatgctctgctcaactgaaggaagacaaatcttgatgatcgctg 901
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Db 241 ATGATGTGGAGCTTGTGAGGATGCTGCTACAGAAGGGCAGACTAACCTTGTGATGATGCAT 300
Qy 902 ttgcactgcactacgctgcgaacattgtgactcccaaaattacaacgagcttttggatc 961
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Db 301 TTGCATTGCACATATGCTGTGTAACAACATGTCGACACAAATAATTACACAGAACTTCTGACA 360
Qy 962 tcgcacttcagatgttataatcatagaaccccaagaggttatactgttcttcacattgctg 1021
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Db 361 TCGCATTGCGGATGTTAAATCTCAGAAACCCAAAGAGGTTACTGTCTTCCATCGCTG 420
Qy 1022 cgaggcgaagagagcgtataaatcatgtctcctt 1056
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Db 421 CTAGGCGGAGAGATCCCTAAATAATTGTTGCTCTTCCTT 455

RESULT 3
LOCUS BG464574 666 bp mRNA EST 20-MAR-2001
DEFINITION EMI_71_D12.g1_A002 Embryo 1 (EM1) Sorghum bicolor cDNA, mRNA
sequence.
ACCESSION BG464574
VERSION BG464574.1 GI:13393216
KEYWORDS EST.
SOURCE sorghum.
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 666)
AUTHORS Reid,S.P., Cordonnier-Pratt,M.-M., Gingle,A. and Pratt,L.H.
TITLE An EST database from Sorghum: developing embryos
JOURNAL Unpublished (2000)
COMMENT Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: PolyTMix
High quality sequence start: 32
High quality sequence stop: 664
POLYA-No.
FEATURES
source
Location/Qualifiers
1..666
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone.lib="Embryo 1 (EM1)"
/note="Organ: Embryos germinated for 24 hr; Vector:
pBluescript II from Lambda Zap II; Site 1: XhoI; Site 2:
EcoRI; The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
BASE COUNT 163 a 160 c 176 g 167 t
ORIGIN
Query Match 10.5%; Score 213.6; DB 154; Length 666;
Best Local Similarity 79.8%; Pred. No. 1.5e-40;
Matches 265; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

Qy 1392 cctgggttctgtgcgaatccacacctctctgaagacacgacgaactgttgatctaatga 1451
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Db 2 CCTTGGTTCTTAATGCTAATCTGCCTACCGAGATTCCAGCGGACA---GTTGACCTGAACGA 58

```

```

QY 1452 aagtccttcataataaagaagaacacttagctcgtgatgacagcactctccaaacagt 1511
DB 111 --AAACATCTCTCGATGTACATAGGCACTTGCACGCGATGATATGAGTTAGTCAACT 168
QY 59 TACTCTTTTCATATGAAGAGAGAGCAGCTTGGCTCGGATGAGAGCCCTAGCCAAACACT 118
QY 1512 ggagctcgggaacgcttttcccgogattgttcgaacgtgctcgaacagatcatgatga 1571
DB 169 TGAACCTCGGGAACAGCTTTCTCCACGGGTCTCAAAAGTCTCGACAAGATCATGATGA 178
QY 1572 tgaactgatcgcgtttccctcgggaagacacagctccgcggaagagagagaggtttca 1631
DB 179 CGAAACCGAGCTGGCTTCCTCGGAGAGACACATCCACAGAGAAGAGAGGAGGTTCCA 238
QY 1632 tgacctgcgagtagttcttcagaagcattccacgaggaagagagagagagaggttc 1691
DB 239 TGACCTGCAAGACTTGGTTTCAAGGCAATTCAGCGAGGACAGGAGGAGACAGCAGTTC 298
QY 1692 ggggctcctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 1723
DB 299 GCGGCGCGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 330

RESULT 4
AV551266 573 bp mRNA EST 06-SEP-2000
LOCUS AV551266 Arabidopsis thaliana roots Columbia Arabidopsis thaliana
DEFINITION cDNA clone RZ123e05R 5', mRNA sequence.
ACCESSION AV551266
VERSION AV551266.1 GI:8722679
SOURCE EST.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 573)
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
20363093
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES
source
1..573
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="RZ123e05R"
/clone_lib="Arabidopsis thaliana roots Columbia"
/tissue_type="roots"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 181 a 104 c 137 g 151 t
ORIGIN

Query Match 10.2%; Score 208.6; DB 31; Length 573;
Best Local Similarity 61.4%; Pred. No. 2.3e-39;
Matches 359; Conservative 0; Mismatches 214; Indels 12; Gaps 1;

QY 683 tcgggtcaacctgacatgattactcttgagaagtcattgctccagatgtttatcaagc 742
DB 1 TCAAGTCTAATGTAGATAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAG 60
QY 743 agattattatcacgccttaagcctcgattattcaccagagaacacagaggtttccta 802
DB 61 AGATAATGTAGACCTAAGACGTGGTTGGAGTACTTAAGTAAG----- 110
QY 803 acaaatgtgaggaggatatacacagagcccttgactctgacgtgtagagtagtcagga 862

```

```

DB 111 --AAACATCTCTCGATGTACATAGGCACTTGCACGCGATGATATGAGTTAGTCAACT 168
QY 863 tctcgtcactgaagagacagacaaatcttgatgctgctgactgacactgacgcgtcg 922
DB 169 TGCCTTTTGAAGAGGATCACACCAATCTAGATGATGCTGTCTCTTTCATTTTCCGCTGTTG 228
QY 923 aacattgactcccaaatcaacacgagcttttgatctcgcacttcagatgttaac 982
DB 229 CATATTGCAATGTGAAGCCGCAACAGATCTTTAAACTTGTATCTTGGCGATGTCAACC 298
QY 983 atagaaaccccaagaggttatactgttcttcacattctcgcagcgagcgaaagagacataaa 1042
DB 289 ATAGGAATCCGAGGGGATATACGGTCTTCATGTTCTCGGATCGGAAGAGGCCACAAT 348
QY 1043 tcatgtctcccttttaacaaaggggctcgaccacagatgttacattcgatggagaa 1102
DB 349 TGATACTATCTCTATTGGAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGAA 408
QY 1103 aagcgggttcaaatctcaaaagactaaacaaaggggattacttctgggttacccgaag 1162
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QY 1223 gggaccacacactcggaagacatcagttctctcttcgaatgagcag 1267
DB 529 GAGACAAATTCCTAGAGATGTTCTCTCCCTCTTTTTCAGTGGCGG 573

RESULT 5
AV160235 613 bp mRNA EST 08-NOV-1999
LOCUS AV160235 L. pennellii trichome, Cornell University Lycopersicon
DEFINITION pennellii cDNA clone CLPT19 similar to A. thaliana transcription
factor inhibitor I kappa B homolog, mRNA sequence.
ACCESSION AV160235
VERSION AV160235.1 GI:6279769
SOURCE EST.
ORGANISM Lycopersicon pennellii.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 613)
Alcala, J., Vrebalov, J., White, R., Matern, A.L., Lakey, J., Holt, I.E.,
Liang, F., Hansen, T.S., Upton, J., Ronning, C.M., Craven, M.B., Fujii,
C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Martin,
G.B., Tanksley, S.D. and Giovannoni, J.
Generation of ESTs from wild tomato (Lycopersicon pennellii)
trichomes
Unpublished (1999)
Contact: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
3 prime sequence.
Location/Qualifiers
1..613
/organism="Lycopersicon pennellii"
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/clone_lib="L. pennellii trichome, Cornell University"
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RESULT	8		
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LOCUS	B26306	629 bp	DNA
			GSS
			13-OCT-1997

DEFINITION	Arabidopsis thaliana genomic clone F18D8, DNA sequence
ACCESSION	F18D8
VERSION	26306.1
KEYWORDS	GT:251272
SOURCE	Arabidopsis thaliana
ORGANISM	thale cress.
	Arabidopsis thaliana
	Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosid II; Brassicales; Brassicaceae; Arabidopsi
REFERENCE	1 (bases 1 to 629)
AUTHORS	Rounsley,S.D., Kelley,J.M., Field,C.E., Craven,M.B., Adams,M.D. and Venter,J.C
TITLE	Use of a BAC End Sequence Database To Identify Minimal Overlaps for Arabidopsis Genomic Sequencing
JOURNAL	Unpublished (1997)
COMMENT	other_GSSs: F18D8TR Contact: Steve Rounsley Department of Eukaryotic Genomics The Institute for Genomic Research

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tel: 301 838 0200
Fax: 301 838 0208
Email: rounsley@tigr.org
Seq primer: M13-21
Class: BAC ends
High quality sequence stop: 629.
Location/Qualifiers
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Produced by Thomas Altmann"
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Db 517 GTAAATTCACAGGCCCTGGATTGAGATGATGTGAGCTGTGGAAGCTCTTTATGACT 458
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Db 397 CGAAAGTGTGTGCGAGATTTCTCTCTGATATGGGTGATGTGGAACCTACAGGAATTC 338
QY 995 gaggttactgtcttcacattctcgaggcgagagagcctaaaattctgtctccc 1054
Db 337 GGGGTTACAGGTTCTTCATTTTCTCGGATGCGGTAGAGAGCCATCATATTATATGCG 278
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RESULT	11
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ACCESSION	AW352680
VERSION	AW352680.1 GI:6851670
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	

QY 1157 ccgaagaagaaacacctctccaaagatagggttatgtattgaaataactggag 1209
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RESULT 14
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 PROTEIN: mRNA sequence.
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 VERSION AW310982.1 GI:6726628
 KEYWORDS EST.
 SOURCE soybean.
 ORGANISM Glycine max
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 REFERENCE 1 (bases 1 to 645)
 AUTHORS Shoemaker,R., Kelm,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Willson,R.
 TITLE Public Soybean EST Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or info@genomesystems.com web site: www.genomesystems.com
 High quality sequence stop: 477.

FEATURES
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 /note="Vector: pT7T3Pac (pT7T3, Pharmacia); Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from mRNA isolated from etiolated hypocotyl tissue of 9-10 day old seedlings. Complementary DNA was synthesized from mRNA using a poly (dT) primer with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and XhoI. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pT7T3-Pac vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker."
 174 a 146 c 128 g 197 t

BASE COUNT 174 a 146 c 128 g 197 t
 ORIGIN

Query Match 6.5%; Score 133.2; DB 114; Length 645;
 Best Local Similarity 57.6%; Pred. No. 2.6e-21;
 Matches 303; Conservative 0; Mismatches 208; Indels 15; Gaps 3;

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QY 1279 cgaggaaggttgctgtatcttgaacaccgagttgcttggcgaagattatgtttccgaig 1338
 DB 573 ACATCAAACTACTGTACCTTGAGAACAGAGTGGCAATTTTGCAAGACTTTTCTTCCTTC 514

QY 1339 gaggcaagagtagcaatggatattgctcaagtggatggaaacttttgaatttaacacctgggt 1398
 DB 513 GAAGCCAAACTAGCCATGGACATTTGGCATGTGTGACACAACATCTCAGTTGTGCTGCTT 454

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 DB 453 TCTGCGTCAAACTCAAAAGGTTCAAAATGGAACCTTAAGGGAGGTTGATCTCAATGAGACT 394

QY 1456 cttttcataatgaagaagaacacttagctcggtgacagcactctccaaaacagtgag 1515
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 DB 333 ATGGGCGGCGCTACTTCCACATTTCTCGGAAGTCTGACAAAGTTTCATGGAGGATGAC 274

QY 1575 --aactgataccggtttccctcggaagacagctccgcggagaag-----aggaag 1623
 DB 273 CTGCGCTGACTTGTTTTACCTTGAAGAGGTTACTTCATGAAGAGCAGAGAAATCAAAAGGACG 214

QY 1624 aggtttcatgactcgagatgttcttcagaagcattccacagcagcagagggagaaat 1683
 DB 213 CGTTTCATGGAGCTTAAGATGACGTCACAAAGGCTTCAACAAAGGACAAAGGCCGAGTTT 154

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 DB 153 AGCCGCTCTGGGATTTTCATCTTCATCATCTCATCTCCCTCAGAG 108

RESULT 15
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 KEYWORDS EST.
 SOURCE soybean.
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
 REFERENCE 1 (bases 1 to 430)
 AUTHORS Shoemaker,R., Kelm,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Willson,R.
 TITLE Public Soybean EST Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or info@genomesystems.com web site: www.genomesystems.com
 Insert Length: 1276 Std Error: 0.00
 Seq primer: -40RP from Gibco
 High quality sequence stop: 406
 POLYA-No.

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 11, 2001, 07:16:22 ; Search time 2704.67 Seconds
(without alignments)
11666.565 Million cell updates/sec

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Perfect score: 2040
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues
Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_ba2:
3: gb_ba3:
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5: gb_in2:
6: gb_in3:
7: gb_om:
8: gb_ov:
9: gb_pat1:
10: gb_pat2:
11: gb_ph:
12: gb_pl1:
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14: gb_pl3:
15: gb_pl4:
16: em_ba1:
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18: em_fun:
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93: gb_pr9:
94: gb_rod:
95: gb_rod2:
96: gb_in4:
97: gb_pr10:
98: em_ba3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	750	36.8	168372	13	AP002746 Oryza sat
C 3	422.2	20.7	2104	14	U76707 Arabidopsis
4	420.6	20.6	2011	9	AR087502 Sequence
5	420.6	20.6	2011	9	AR087503 Sequence
6	411.8	20.2	1608	9	AR087505 Sequence
7	409.2	20.1	1597	9	AR087504 Sequence
8	400.4	19.6	1194	9	AR087506 Sequence


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55224	TCTTATCTGTGCAACTTATGCAACAAATCTTGCATGAAACTCTTGAAGATGCCTTG	55165	Db	55224
674	ataggtagtcctcgtcaaaccttgacatgattactcttgagaagctattcctccagatg	733	QY	674
55164	ATATGGTAGTCCGGTCAAACTTGCATGATGATCTCTTGAAGATGATGCTCTCCAGATG	55105	Db	55164
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JOURNAL Submitted (30-OCT-1996) DCMB Group, Botany, Duke University, LSRC Building, Research Dr., Durham, NC 27708-1000, USA

FEATURES

source Location/Qualifiers
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Best Local Similarity 59.88; Pred. No. 1.6e-36;
Matches 715; Conservative 0; Mismatches 466; Indels 15; Gaps 2;

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ACCESSION	AX049426		
VERSION	AX049426.1	GI:12226154	
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ORGANISM	Oryza sativa		
REFERENCE	1 (bases 1 to 1428)		
AUTHORS	Bougrit,O.V., Rommens,C.M., Srivastava,N. and Swords,K.M.		
TITLE	Acquired resistance genes in plants		
JOURNAL	Patent: WO 0070069-A 1 23-NOV-2000;		
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RESULT 11
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PAT      23-NOV-2000
DEFINITION Sequence 1 from Patent WO065037.
ACCESSION AX041006
VERSION    AX041006.1 GI:11340602
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            Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
            Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 2154)
            Crane,E.H., Rice,D.A., Simmons,C.R., Tossberg,J.T., Sandahl,G.A.
            and Zhang,L.
            Maize nr1 polynucleotides and methods of use
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LOCUS	AX049431 1830 bp DNA PAT 12-JAN-2001
DEFINITION	Sequence 6 from Patent WO070069.
ACCESSION	AX049431
VERSION	AX049431.1 GI:12226158
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ORGANISM	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Triticeae; Triticum. Triticum.
REFERENCE	1 (bases 1 to 1830)
AUTHORS	Bouqir,O.V., Rommens,C.M., Srivastava,N. and Swords,K.M.

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 Db 1627 GCGATGCAAAATTGGCAAGCAGACATCACACCAGAAAGTTGGTGGTTTTCTGCGAGCAAGT 1686
 Qy 1411 ccacctctgaaagacacacggaactgttgatctaaatgaaagtccctttcataatgaaa 1470
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 Qy 1531 ttcccgcgatgttcgaacgtgtctcgacaagatcatggatgatg 1573
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Search completed: July 11, 2001, 09:09:33
 Job time: 8791 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 11, 2001, 07:21:13 ; Search time 102.79 seconds
(without alignments)
3676.730 Million cell updates/sec

Title: US-09-294-539-3
Perfect score: 2040
Sequence: 1 atggagccgacgacgacga.....caaaaaaaaaaaaaaaaaa 2040

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 317530 seqs, 92630169 residues

Total number of hits satisfying chosen parameters: 635060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.NA.*
1: /cgn2.6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2.6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2.6/ptodata/1/ina/6A_COMB.seq.*
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5: /cgn2.6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cgn2.6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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4	420.6	20.6	2011	3	US-08-996-685-7
5	411.8	20.2	1608	2	US-08-989-478-11
6	411.8	20.2	1608	3	US-08-996-685-11
7	409.2	20.1	1597	2	US-08-989-478-9
8	409.2	20.1	1597	3	US-08-996-685-9
9	400.4	19.6	1194	2	US-08-989-478-13
10	400.4	19.6	1194	3	US-08-996-685-13
11	264.8	13.0	786	2	US-08-989-478-15
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13	258.4	12.7	5655	2	US-08-989-478-1
14	258.4	12.7	5655	3	US-08-996-685-1
15	258.4	12.7	5655	3	US-08-880-179-2
16	258.4	12.7	9919	3	US-08-880-179-1
17	81	4.0	4257	2	US-08-690-473-1
18	81	4.0	4257	4	US-09-259-821A-1
19	81	4.0	4257	4	US-08-843-659-1
20	81	4.0	12001	1	US-08-458-568A-11
21	79.2	3.9	1931	3	US-09-130-114-2
22	75.6	3.7	1138	3	US-08-581-148C-3
23	75.2	3.7	390	4	US-09-197-649-7
24	74.6	3.7	390	4	US-09-197-649-7
25	74.4	3.6	459	2	US-08-387-942C-9
26	74.4	3.6	38506	4	US-09-320-878-19
27	73.6	3.6	44377	2	US-08-804-227C-7

28	73.6	3.6	44377	2	US-08-804-198-1	Sequence 1, Appl
29	72.6	3.6	645	2	US-08-403-852D-9	Sequence 9, Appl
30	72.6	3.6	645	3	US-08-510-648B-9	Sequence 9, Appl
31	72.6	3.6	645	4	US-09-231-818-9	Sequence 9, Appl
32	70.6	3.5	784	1	US-08-392-731-1	Sequence 1, Appl
33	69.6	3.4	2312	1	US-07-736-178C-1	Sequence 1, Appl
34	69.2	3.4	1320	2	US-08-461-775-8	Sequence 8, Appl
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36	69.2	3.4	1620	2	US-08-461-775-10	Sequence 10, Appl
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38	68.2	3.3	1845	4	US-09-029-603-5	Sequence 5, Appl
39	67.8	3.3	1485	1	US-08-471-601-23	Sequence 23, Appl
40	67.8	3.3	1485	1	US-08-474-556-23	Sequence 23, Appl
41	67.8	3.3	1485	1	US-08-479-382-23	Sequence 23, Appl
42	67.8	3.3	1485	1	US-08-470-354-23	Sequence 23, Appl
43	67.8	3.3	1485	1	US-08-479-383-23	Sequence 23, Appl
44	67.8	3.3	1485	2	US-08-479-041-23	Sequence 23, Appl
45	67.8	3.3	5970	4	US-09-320-878-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-989-478-6
; Sequence 6, Application US/08989478
; Patent No. 5986082
; GENERAL INFORMATION:
; APPLICANT: Uknes, Scott
; APPLICANT: Hunt, Michelle
; APPLICANT: Steiner, Henry-York
; APPLICANT: Ryals, John
; TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
; TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSER: No. 5986082artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 5986082th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,177
; FILING DATE: 13-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,379
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,382
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,730
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,021
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,022
; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2011 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..2011
OTHER INFORMATION: /note= "NIM1 cDNA sequence"
NAME/KEY: CDS
LOCATION: 43..1824
OTHER INFORMATION: /product= "NIM1 protein"
US-08-989-478-6

Query Match 20.6%; Score 420.6; DB 2; Length 2011;

Best Local Similarity 56.0%; Pred. No. 2.2e-82;

Matches 979; Conservative 0; Mismatches 704; Indels 66; Gaps 7;

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DB 91 ACTAGTTTCGTCGACGATACACGACCTCTCTATTTATCTGGCCGCCGACAA 150
QY 73 gccagcggcggcggcggcggcggcggcggcggcggcggcggcggcggcggcggcggc 132
DB 151 GTACTACCGGACCTGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 210
QY 133 ttccgctccgaggaactcgtctcctccgacggcgacggcgacggcgacggcgacggcg 192
DB 211 TTTGACTCGCGGATGATTC-----TACAGCGACGCTTAAGCTTGT 252
QY 193 ggcggcggcggcggcggcggcggcggcggcggcggcggcggcggcggcggcggcggc 252
DB 253 CTCCTCCGACGGCGGGAAGTTTCTTCCACCGGTGCGTTTGTACGAGAGCTCTTTTC 312
QY 253 ctgcgcgcgtcttcgc 312
DB 313 TCAAGAGCGCTTAGC-----CGCCGCTAAGAGGAGAAAGACTCCAACACACGCC 366
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DB 367 GCCGTGAAGCTCGAGCTTAAGGAGAT-----TGCCAAAGATTACGAAGTCGGT 414
QY 373 tacgagcgcgtcggcgtgctgctgaactacactcctacagcgcgcgcgcgcgcgcgcgcgc 432
DB 415 TTCGATTTCGTTGTCACGTTTGTGCTTATGTTTACACAGCAGAGAGTGTGAGACCGCGCT 474
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DB 535 GATTTCATGTTGGAGGTTCTCTATTGTCCTTTCATCTTCAAGATCCCTGAATTAATTACT 594
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DB 595 CTCATACAGGACCTTATTGACCTTTGACACAAAGTTGTTATAGAGGACACATTTGTT 654
QY 613 atctatctgttgcaacttatgcaacaattcttgcataaactcgttgaagatgcctt 672
DB 655 ATACTCAAGCTTGCTTAATATATGTTGTAAGCTTGTATGAAGCTTATGATAGATGATAA 714
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DB 715 GAGATTATTGTCGAAGCTTAATGTAGATATGTTAGTCTTTGAAAGATCAFTTGGCGGAAGAG 774
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DB 775 CTTGTTAAAGAGATAATTGATGACGTAAAGACCTTGGTTGGAGGTACCTTAAGTAAG 834
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DB 835 -----AAACATGTCGTAATGTACATAAGSCACTTGACTCGGATGATATTGAG 882
QY 853 ctagtccaggatgctgctcactgaagacagacaaactcttgatgatcgcttggcactgcac 912
DB 883 TTAGTCAAGTTGCTTTTGAAGAGGATACACCAATAGATGATGCTGCTCTTTCAT 942
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QY 1033 gacctaataatcattgtcctcctttaaaccaggggctcgaccagcagatgttacattc 1092
DB 1063 GAGCCACAAATTGATCTATCTATTGGAAGAGGTGCAAGTGCATCGAAGCAACTTTG 1122
QY 1093 gatgggagaaagcggttcaaatctcaaaagactcaaaacaaaggggactcttcttgg 1152
DB 1123 GAAGGTAGACCGCACTCATGATCGCAAAACACAGCCACTATGGCGTTGAATGTAATAAT 1182
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DB 1243 GAAGCAAAAGAGAACTTCTTCTAGAGATGTTCTCTCCCTCTTTTGGCGTGGCGCGCAT 1302
QY 1273 agtctagagggaaggttctgtatcttgaacccaggttgccttggcgaagattatgtt 1332
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QY 1450 gaaagtccttctcaatgaagaagaacacttagctcggatgacagcactctccaaaca 1509
DB 1483 ATAGCAGCTTTCAGATCTTAGAAGAGCATCAAAAGTAGACTTAAAGAGGCTTTCTTAAACC 1542
QY 1510 gtgagctcgggaaacgcttttcccgatgttcgaactgctcgaacagatcatg--- 1566
DB 1543 GTGAACCTCGGAACAGATTTCTCCCGCTGTTTGGCAGTCTCGACCATGATATGAAC 1602
QY 1567 ---gatgatgaactgatccggttttccctcggaaagacacgctccgcg-----gag 1614
DB 1603 TGTGAGGACTTGTACTCACTGCTTGGGAGAGACGACACTGCTGAGAAACGACTACAA 1662
QY 1615 aagagggaaggtttcatgacctcaggatgttcttcagaaggcattccacagagacaag 1674
DB 1663 AAGAAGCAAGGTACATGGAATAACAGAGACACTAAGAAGAGGCTTTTAGTGAGGACAA 1722
QY 1675 gagagaatcacaggtcggggctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1734
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QY 1735 cgaccaag 1743
DB 1783 GGAAAGAGG 1791

RESULT 2

US-08-989-478-7
; Sequence 7, Application US/08989478
; Patent No. 5986082
; GENERAL INFORMATION:
; APPLICANT: Uknes, Scott
; APPLICANT: Hunt, Michelle
; APPLICANT: Steiner, Henry-York
; APPLICANT: Ryals, John
; TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
; DISEASE RESISTANCE IN PLANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5986082artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 5986082th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,177
; FILING DATE: 13-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,379
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,382
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,730
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,021
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,022
; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-21214/PI/CGC1911
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..1824
; OTHER INFORMATION: /product= "altered form of NIM1"
; OTHER INFORMATION: /note= "Serine residues at amino acid positions 55 and 59 in
; OTHER INFORMATION: wild-type NIM1 gene product have been changed to Alanine
; OTHER INFORMATION: residues."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 205..217
; OTHER INFORMATION: /note= "nucleotides 205 and 217

; OTHER INFORMATION: changed from T's to G's compared to wild-type sequence."
US-08-989-478-7

Query Match 20.6%; Score 420.6; DB 2; Length 2011;
Best Local Similarity 56.0%; Pred. No. 2.2e-82;
Matches 979; Conservative 0; Mismatches 704; Indels 66; Gaps 7;
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DB 91 ACTAGTTTCGTCGTACCGATACACCGACTCTCTATTGTTTATGTCGCCGCCGCAACA 150
QY 73 gcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcg 132
DB 151 GTACTCACCGGACCTGATGTAATCTGCTCTCAATTCTCTCCAACAGCTTCGAAGCGGTC 210
QY 133 ttccgctcccgagagacttcgcttcctccgacgagcgagcgagcgagcgagcgagcg 192
DB 211 TTTGACGCGCGGATGATTTC-----TACAGCGACGCTAAGCTTGT 252
QY 193 ggcggcgcgcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgag 252
DB 253 CTCCTCCGACGCGCGGAAAGTTCTTTCCACCGGCTGTTTGTACGCGAAGACTCTTTC 312
QY 253 ctgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgag 312
DB 313 TTCAAGAGCGCTTAGC-----CGCCGCTAAGAGAGAGAT-----TGCCAAAGGATTACGAAGTCGGT 366
QY 313 agcgagagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcg 372
DB 367 GCGGTGAAGCTCGAGCTTAAGGAGAT-----TGCCAAAGGATTACGAAGTCGGT 414
QY 373 tacgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgag 432
DB 415 TTCGATTTCGTTGTTGAGTGTGTTTGGCTTATGTTTACAGCAGCAGAGTGAACCGCCCT 474
QY 433 aagggcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgag 492
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QY 493 gcggtcagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcg 552
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QY 733 gttatcaagcagattatgatgcacccctaagcctcgagattattaccagaaaaaaga 792
DB 775 CTGTGTTAAAGAGATAATGATAGACGCTAAGAGCTTGGTTTGGAGGTACCTAAGTAAAG 834
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QY 853 ctagtccagtgctgctcactgaagagacagacaaatcttgatgatcggtttgcaactgcac 912
DB 883 TTAGTCAAGTTGCTTTTGAAGAGGATGACACCAATCTAGATGATGCTGCTCTTCAT 942
QY 913 tacgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgag 972
DB 943 TTCGCTGTTGCATATTGCAATGTGAAGACCGCAACAGATCTTTTAAACCTTGTATCTGCC 1002
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RESULT

Query Match 20.6%; Score 420.6; DB 3; Length 2011;
Best Local Similarity 56.0%; Pred. No. 2.2e-82;
Matches 979; Conservative 0; Mismatches 704; Indels 66;

ADDRESSEE: No. 6031153artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6031153th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,685
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/761,543
FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,378
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,024
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/875,015
FILING DATE: 16-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21215/PI/CGC1912
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2011 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
ORGANISM SOURCE:
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1..2011
OTHER INFORMATION: /note= "NM1 cdna sequence"
NAME/KEY: CDS
LOCATION: 43..1824
OTHER INFORMATION: /product= "NM1 protein"
PS-08-996-685-6

Seq. ID	Seq. Name	Length	Matches	Mismatches	Indels	Gaps
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2	Seq2	100	85	15	0	0
3	Seq3	100	82	18	0	0
4	Seq4	100	80	20	0	0
5	Seq5	100	78	22	0	0
6	Seq6	100	75	25	0	0
7	Seq7	100	72	28	0	0
8	Seq8	100	70	30	0	0
9	Seq9	100	68	32	0	0
10	Seq10	100	65	35	0	0
11	Seq11	100	62	38	0	0
12	Seq12	100	60	40	0	0
13	Seq13	100	58	42	0	0
14	Seq14	100	55	45	0	0
15	Seq15	100	52	48	0	0
16	Seq16	100	50	50	0	0
17	Seq17	100	48	52	0	0
18	Seq18	100	45	55	0	0
19	Seq19	100	42	58	0	0
20	Seq20	100	40	60	0	0
21	Seq21	100	38	62	0	0
22	Seq22	100	35	65	0	0
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6
RESULT
US-08-996-685-11
; Sequence 11, Application US/08996685
; Patent No. 6031153
; GENERAL INFORMATION:
; APPLICANT: Ryals, John
; APPLICANT: Friedrich, Leslie
; APPLICANT: Uknes, Scott
; APPLICANT: Molina, Antonio
; APPLICANT: Russ, Wilhelm
; APPLICANT: Knauf-Beiter, Gertrude
; APPLICANT: Kung, Ruth
; APPLICANT: Kessmann, Helmut
; APPLICANT: Oostendorp, Michael
; TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 6031153artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6031153th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,685
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/761,543
; FILING DATE: 6-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,378
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,379
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,382
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,730
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,021
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,022
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,024
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/875,015
; FILING DATE: 16-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-21215/Pl/COC1912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1608 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

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Qy 1396 ---ggtctgtgcaaatccacctctgaaagacacggaacactgtgtatctaaatgaa 1452
Db 1012 ACTAGCCTCGAGCCTGACCGTCTCACTGGTACGAGAGACATCACCGGGTGTAAAGATA 1071
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Qy 1738 ccaagg 1743
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RESULT 9
US-08-989-478-13
; Sequence 13, Application US/08989478
; Patent No. 5986082
; GENERAL INFORMATION:
; APPLICANT: Uknes, Scott
; APPLICANT: Hunt, Michelle
; APPLICANT: Steiner, Henry-York
; APPLICANT: Ryals, John
; TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
; TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5986082artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 5986082th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,177
; FILING DATE: 13-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,379
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,382
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,730
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/035,021
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,022
; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1194 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1194
; OTHER INFORMATION: /product= "Altered form of NIM1"
; OTHER INFORMATION: /note= "N-terminal/C-terminal chimera."
; US-08-989-478-13

Query Match 19.6%; Score 400.4; DB 2; Length 1194;
Best Local Similarity 59.8%; Pred. No. 4.4e-78;
Matches 715; Conservative 0; Mismatches 466; Indels 15; Gaps 2;
Qy 376 gagcgctgcggtgctgcgactacctacagcgccgcgctgcgagcctgcccaag 435
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Db 64 GGAGTTTCTGAATCGCAGACGAGAAATGCTGCCACGCTGGCTTCCCGCGCGGTGGAT 123
Qy 496 tteatggcgaagtccttcctgcgcctccacgttcaggtccgagctccacacactc 555
Db 124 TTCAATGTTGGAGGTTCTCTATTTGGCTTTCATCTTCAAGATCCCTGAATTAATTTACTCTC 183
Qy 556 tccagcgcgctcctctgctgctgctgataaggttgaagtagataaacctctctattgatc 615
Db 184 TATCAGAGGCACCTTATTGGACGTTGTAGACAAAGTTGTATAGAGGACACATTTGGTTATA 243
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Db 532 GCTGTTGCATATTGCAATGTGAAGACCGCAACAGATCTTTTAAACATTTGATCTTCCCGAT 591
Qy 976 gtaatcatagaaccccaagggttatactgtcttctcattgctgcgagggcgaagagag 1035


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Qy 1096 gggagaaagggttcaaatctcaaaagacaaacaaagggtattacttgggtt 1155
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RESULT 10
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; Sequence 13, Application US/08996685
; Patent No. 6031153
; GENERAL INFORMATION:
; APPLICANT: Ryals, John
; APPLICANT: Friedrich, Leslie
; APPLICANT: Uknes, Scott
; APPLICANT: Molina, Antonio
; APPLICANT: Ruess, Wilhelm
; APPLICANT: Knauf-Belter, Gertrude
; APPLICANT: Kung, Ruth
; APPLICANT: Kessmann, Helmut
; APPLICANT: Oostendorp, Michael
; TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSER: No. 6031153artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6031153th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,685
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/761,543

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; FILING DATE: 6-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,378
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,379
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,382
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,730
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,021
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,022
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,024
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/875,015
; FILING DATE: 16-JUL-1997
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1194 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1194
; OTHER INFORMATION:
; OTHER INFORMATION: /note="Altered form of NTM1"
; OTHER INFORMATION: /note="N-terminal/C-terminal chimera."
US-08-996-685-13

Query Match 19.6%; Score 400.4; DB 3; Length 1194;
Best local Similarity 59.8%; Pred. No. 4,4e-78;
Matches 715; Conservative 0; Mismatches 466; Indels 15; Gaps 2;

Qy 376 gagcgctgcgctgtgtcgtcgaactaccctcagcggccgcgctgcgagctgccaaag 435
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Db 532 GCTGTGATATTCGATATGTGAGAGACCCCAACAGATCTTTTAAACCTGATCTTGCCGAT 591
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RESULT 11
US-08-989-478-15
: Sequence 15, Application US/08989478
: Patent No. 5986082
: GENERAL INFORMATION:
: APPLICANT: Uknes, Scott
: APPLICANT: Hunt, Michelle
: APPLICANT: Steiner, Henry-York
: APPLICANT: Ryals, John
: TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
: TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
: NUMBER OF SEQUENCES: 32
: CORRESPONDENCE ADDRESS:
: ADDRESS: No. 5986082art1s Corporation

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STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 5986082th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,478
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SRO ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..786
OTHER INFORMATION:
OTHER INFORMATION: /note="Ankyrin domains of NIM1."
US-08-989-478-15

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Query Match 13.0%; Score 264.8; DB 2; Length 786;
Best Local Similarity 60.8%; Pred. No. 9e-49;
Matches 456; Conservative 0; Mismatches 282; Indels 12; Gaps 1;

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US-08-996-685-15
 12
 Sequence 15, Application US/08996685
 Patent No. 6031153
 GENERAL INFORMATION:
 APPLICANT: Ryals, John
 APPLICANT: Friedrich, Leslie
 APPLICANT: Uknes, Scott
 APPLICANT: Molina, Antonio
 APPLICANT: Ruess, Wilhelm
 APPLICANT: Knauf-Belter, Gertrude
 APPLICANT: Kung, Ruth
 APPLICANT: Kessmann, Helmut
 APPLICANT: Oostendorp, Michael
 TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 6031153artls Corporation
 STREET: 3054 Cornwallis Road
 CITY: Research Triangle Park
 STATE: No. 6031153ch Carolina
 COUNTRY: USA
 ZIP: 27709
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/996,685
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/761,543
 FILING DATE: 6-DEC-1996

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RESULT 13
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 Patent No. 5986082
 GENERAL INFORMATION:
 APPLICANT: Uknes, Scott
 APPLICANT: Hunt, Michelle
 APPLICANT: Steiner, Henry-York
 APPLICANT: Ryals, John
 TITLE OF INVENTION: ALTERED FORMS OF THE NINI GENE CONFERRING
 TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 5986082art's Corporation
 STREET: 3054 Cornwallis Road
 CITY: Research Triangle Park
 STATE: No. 5986082th Carolina
 COUNTRY: USA
 ZIP: 27709
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/989,478
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/033,177
 FILING DATE: 13-DEC-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/034,379
 FILING DATE: 27-DEC-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/034,382
 FILING DATE: 27-DEC-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/034,730
 FILING DATE: 10-JAN-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/035,021
 FILING DATE: 10-JAN-1997

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1 PRIOR APPLICATION DATA:
2 APPLICATION NUMBER: US 60/035,022
3 FILING DATE: 10-JAN-1997
4 ATTORNEY/AGENT INFORMATION:
5 NAME: Melgs, J. Timothy
6 REGISTRATION NUMBER: 38,241
7 REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
8 TELECOMMUNICATION INFORMATION:
9 TELEPHONE: (919) 541-8587
10 TELEFAX: (919) 541-8689
11 INFORMATION FOR SEQ ID NO: 1:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 5655 base pairs
14 TYPE: nucleic acid
15 STRANDEDNESS: single
16 TOPOLOGY: linear
17 MOLECULE TYPE: DNA (genomic)
18 HYPOTHETICAL: NO
19 ANTI-SENSE: NO
20 FEATURE:
21 NAME/KEY: exon
22 LOCATION: 2787..3347
23 OTHER INFORMATION: /product= "1st exon of NIM1"
24 FEATURE:
25 NAME/KEY: exon
26 LOCATION: 3427..4162
27 OTHER INFORMATION: /product= "2nd exon of NIM1"
28 FEATURE:
29 NAME/KEY: exon
30 LOCATION: 4271..4474
31 OTHER INFORMATION: /product= "3rd exon of NIM1"
32 FEATURE:
33 NAME/KEY: exon
34 LOCATION: 4586..4866
35 OTHER INFORMATION: /product= "4th exon of NIM1"
36 FEATURE:
37 NAME/KEY: CDS
38 LOCATION: John(2787..3347, 3427..4162, 4271..4474, 4586..4866)
39 US-08-989-478-1

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Qy 614	tcttctcgttgccacctatgcaacaactctgtcagaaactgttgaaactgttgaaagtgcctg	673		
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Qy 674	ataatgtagtcgcgcgtcaaacaccttgacagattaccctcttgagaagtcattgcctccagatg	733		
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RESULT 14

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US-08-996-685-1
: Sequence 1, Application US/08996685
: Patent No. 6031153
: GENERAL INFORMATION:
: APPLICANT: Ryals, John
: APPLICANT: Friedrich, Leslie
: APPLICANT: Ryals, John
: APPLICANT: Kunes, Scott
: APPLICANT: Molina, Antonio
: APPLICANT: Ruess, Wilhelm
: APPLICANT: Knauf-Belter, Gertrude
: APPLICANT: Kung, Ruth
: APPLICANT: Kessmann, Helmut
: APPLICANT: Oostendorp, Michael
: TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
: NUMBER OF SEQUENCES: 32
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 6031153artis Corporation
: STREET: 3054 Cornwallis Road
: CITY: Research Triangle Park
: STATE: No. 6031153th Carolina
: COUNTRY: USA
: ZIP: 27709
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/996,685
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/761,543
: FILING DATE: 6-DEC-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/034,378
: FILING DATE: 27-DEC-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/034,379
: FILING DATE: 27-DEC-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/034,382
: FILING DATE: 27-DEC-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/034,730
: FILING DATE: 10-JAN-1997
: PRIOR APPLICATION DATA:

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: APPLICATION NUMBER: US 60/035,021
: FILING DATE: 10-JAN-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/035,022
: FILING DATE: 10-JAN-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/035,024
: FILING DATE: 10-JAN-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/875,015
: FILING DATE: 16-JUL-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Meigs, J. Timothy
: REGISTRATION NUMBER: 36,241
: REFERENCE/DOCKET NUMBER: PF/5-21215/PI/CGC1912
: TELEPHONE: (919) 541-8587
: TELEFAX: (919) 541-8689
: INFORMATION FOR SEQ. ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5655 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: exon
: LOCATION: 2787..3347
: OTHER INFORMATION: /product= "1st exon of NIM1"
: FEATURE:
: NAME/KEY: exon
: LOCATION: 3427..4162
: OTHER INFORMATION: /product= "2nd exon of NIM1"
: FEATURE:
: NAME/KEY: exon
: LOCATION: 4271..4474
: OTHER INFORMATION: /product= "3rd exon of NIM1"
: NAME/KEY: exon
: LOCATION: 4586..4866
: OTHER INFORMATION: /product= "4th exon of NIM1"
: NAME/KEY: CDS
: LOCATION: join(2787..3347, 3427..4162, 4271..4474, 4586..4866)
US-08-996-685-1

Query Match 12.7% Score 258.4; DB 3; Length 5655;
Best Local Similarity 60.0%; Pred. No. 4,6e-47;
Matches 455; Conservative 0; Mismatches 291; Indels 12; Gaps 1;

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QY 614 tcttattcgttgcacattatgaacaaactcttgcattgaactgttgaagaatgcctg 673
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QY 674 atatgtagtcgcggtcaaaccttgacatgattctcttggaagatgattccctccagatg 733
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Search completed: July 11, 2001, 09:05:58
 Job time: 6285 sec

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	16	400.4	19.6	1194	19	AAV46278	A. thaliana C- and
	17	400.4	19.6	1194	19	AAV43664	Non-inducible immu
	18	381.8	18.7	1740	21	AAA97192	B. napus NtM1 homo
	19	380.4	18.6	1603	21	AAA97203	A. thaliana NtM1 h
	20	380.4	18.6	1618	21	AAA97233	A. thaliana NtM1 h
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	23	317.2	15.5	2069	21	AAA61048	Rice putative negat
	24	315.8	15.5	1428	22	AAAC84339	Rice Nph1 protein
	25	315.8	15.5	2368	22	AAAC84340	Rice NPH1 cDNA seq
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	28	309.8	15.2	1830	22	AAAC84343	Wheat Nph2-2 protee
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	30	306.2	15.0	1824	22	AAAC84342	Wheat Nph2-1 cDNA
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	33	276.6	13.6	498	21	AAA97216	B. vulgaris NtM1 h
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	39	258.4	12.7	5655	19	AAV46273	A. thaliana NtM-1
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ALIGNMENTS

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AC	AAAC81457:	
DT	28-FEB-2001 (first entry)	
XX		
DE	Rice NPR1 homologue 1 (NtM1) cDNA, SEQ ID NO:3.	
KW	Rice; NtM1; NPR1 homologue 1; PNI interactor; SAR; bzIP protein;	
KW	systemic acquired resistance; Yeast two-hybrid system; transgenic plant;	
KW	pathogen resistance; virus; bacterium; nematode; fungus; insect; ss.	
OS	Oryza sativa.	
PN	WO200063417-A2.	
XX		
PD	26-OCT-2000.	
XX		
PF	06-APR-2000; 2000MO-USO9060.	
XX		
PR	19-APR-1999; 99US-0294539.	
XX		
PA	(REGC) UNIV CALIFORNIA.	
XX		
PI	Chern MS, Ronald P;	
XX		
DR	WPI; 2001-090867/10.	
DR	P-PDB; AAB29750.	
XX		

Noval nucleic acid construct for enhancing pathogen resistance, encodes
rice proline rich NPR1 interactor proteins, polypeptides interacting
with PNI or MN1, and bzIP protein interacting with Arabidopsis NPR1 -

OY	1681	aatgcgaaggtcggggtcttcgtgtgtgtcgaatcgacatcggtccggtcattcgacca	1740
OY	1681	aatgcgaaggtcggggtcttcgtgtgtgtcgaatcgacatcggtccggtcattcgacca	1740
Db	1681	aatgcgaaggtcggggtcttcgtgtgtgtcgaatcgacatcggtccggtcattcgacca	1740
OY	1741	aggagaatgaaccacattgtctcccacaataagtgtgccatatgatagctaactgtctccttg	1800
Db	1741	aggagaatgaaccacattgtctcccacaataagtgtgccatatgatagctaactgtctccttg	1800
OY	1801	agctactcaccttgaatgttgttcctctctgtcaattgtccccccaataataatctcgaatgttt	1860
Db	1801	agctactcaccttgaatgttgttcctctctgtcaattgtccccccaataataatctcgaatgttt	1860
OY	1861	aggctttgtaacatgattagtctttacacgcatctttgccccgttaattgttgaacgcagaagt	1920
Db	1861	aggctttgtaacatgattagtctttacacgcatctttgccccgttaattgttgaacgcagaagt	1920
OY	1921	tcaactagtcttctgtactcgaagtgataaacaaagtgccttgaatttgaatgtgtacttgaa	1980
Db	1921	tcaactagtcttctgtactcgaagtgataaacaaagtgccttgaatttgaatgtgtacttgaa	1980
OY	1981	tttccagtggttctgtcgcgttaaaaaatgagatgatttcttggcaaaaaaaaaaaaaaaa	2040
Db	1981	tttccagtggttctgtcgcgttaaaaaatgagatgatttcttggcaaaaaaaaaaaaaaaa	2040

RESULT 2

AAAG61047	standard; cDNA; 2194 BP.
ID	AAAG61047
AC	AAAG61047;
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DT	12-OCT-2000 (first entry)
DE	Rice putative negatively phytochrome regulated 1 (NPRI) gene #1.
XX	
KW	Rice: negatively phytochrome regulated 1 gene; NPRI:
KN	systemic acquired resistance; gene mapping; transgenic plant; ss.
XX	
OS	Oryza sativa.
XX	
FH	Key Location/Qualifiers
FT	CDS 140..1876
ET	/ftag= a
FT	/product= "NPRI"
PN	
XX	
PD	MO200028036-A2.
XX	
PD	18-MAY-2000.
XX	
XX	04-NOV-1999; 99WO-US25953.
PF	
PR	05-NOV-1998; 98US-0107242.
XX	
PPA	(DUPO) DU PONT DE NEMOURS & CO E I.
XX	
P1	Famodu OO, Fang Y, Liu Z, Miao G, Odeh JT;
DR	MPR: 2000-451636/39.
XX	
DR	P-PSDB: AAB09875.
PT	Isolated nucleic acid fragments encoding an NPRI gene which can be used
XX	
PT	to transform plants and provide disease resistance -
XX	
PS	Claim 2; Page 29; 35pp; English.
CC	

The present sequence is a putative version of the rice negatively phytochrome regulated 1 (NPRI) gene coding sequence. It was isolated by screening a leaf cDNA library for those sequences which were involved in the NPRI gene from Arabidopsis thaliana. The protein is created transgenic plants which are protected from pathogens. It can also be used to find homologous sequences in other plants which have a similar effect.

[illegible]

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Db 1088 ctcgacttcgacgagatgaatcatatgaataaccgaaggtatcagttcttcaacttct 1147
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Db 1148 gcgagcgcaagaagagcctaaatcatgtctccctttaaccaagggtctcgacacga 1207
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Oy 1321 aggaatgatgtccgagtgaggaagtagcaatgatgtctcaagtgagtgaaact 1380
Db 1448 aggaatgatgtccgagtgaggaagtagcaatgatgtctcaagtgagtgaaact 1507
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Db 1508 ttggaatgaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1567
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Db 1568 gatccaatgaagaagctcttcaataatgaagaagacactatgctcggatgacacac 1627
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Oy 1621 aagaggttcacatgacatgacagatgtcttccagaagacatccacagagacagaagg 1680
Db 1748 aagaggttcacatgacatgacagatgtcttccagaagacatccacagagacagaagg 1807
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Db 1808 aatgcaagctcgggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1867
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Db 1868 aggaataaacaacatgctcccaataatgttgcacatgacatgacatgacatgacatg 1927
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RESULT 3

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AAA97191
ID AAA97191 standard; cDNA: 1731 BP.
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AC AAA97191;
XX
DT 25-JAN-2001 (first entry)
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DE L. esculentum NIM1 homologue coding sequence SMQ ID NO: 3.
XX
XX Systemic acquired resistance; SAR; signal transduction cascade;
XX disease resistance; tobacco; tomato; canola; sunflower; sugarbeet;
XX potato; ss.
XX
OS Lycopersicon esculentum.
XX
FH Key Location/Qualifiers
FT CDS 1..1731
FT /tag= a
FT /product= "NIM1 homologue"
XX
XX MO200053762-A2.
XX
XX 14-SEP-2000.
XX
XX 07-MAR-2000; 2000WO-EP01978.
XX
XX 09-MAR-1999; 99US-0265149.
XX
XX (NOVS ) NOVARTIS AG.
XX (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
XX Salmeron JM, Weislo LJ, Willits MG, Mengiste T;
XX
XX WPI: 2000-594322/56.
XX P-PSDB; AAB27302.
XX
XX Novel plant genes for enhancing systemic acquired resistance gene
XX expression and broad spectrum disease resistance in plants, are
XX homologues of Arabidopsis NIM1 gene -
XX
XX Claim 3: Page 73-75; 152pp; English.
XX
XX
XX The present invention is concerned with the isolation of NIM1 homologues
XX and their coding sequences from Arabidopsis thaliana, Brassica napus,
XX Nicotiana tabacum, Lycopersicon esculentum, Beta vulgaris, Helianthus
XX annuus and Solanum tuberosum. NIM1 is one of the proteins involved in the
XX signal transduction cascade leading to systemic acquired resistance (SAR)
XX in plants. This gives the plants an increased resistance to disease. The
XX gene and protein can be used to produce transgenic plants resistant to
XX diseases caused by viruses, such as tobacco or cucumber mosaic virus,
XX ringspot virus, pelargonium leaf curl virus, red clover mottle virus,
XX tomato bushy stunt virus, fungi, including Phytophthora parasitica and
XX Petronospora tabacina, bacteria such as Pseudomonas syringae and P.
XX tabaci, insects, including aphids and lepidoptera and nematodes such as
XX Meloidogyne incognita. In particular they can be used against disease
XX organisms of maize.
XX
XX Sequence 1731 BP; 508 A; 318 C; 408 G; 497 T; 0 other:
XX
XX
XX Query Match 28.9%; Score 590.2; DB 21; Length 1731;
XX Best Local Similarity 65.2%; Pred. NO. 1.4e-89;
XX Matches 906; Conservative 0; Mismatches 468; Indels 15; Gaps 2;
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Db 308 aagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 367
Oy 416 ggtgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 475
Db 368 aagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 427
Oy 476 gttgcaccccgctcgttcacatgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 535

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Db 428 ctgttaggcagcgtgtggtcccttcattgttcagggtttgtgacgcaccccttcattcaga 487
QY 536 tcgcgcagctcaccaccccttcaccgcggtctccttgatctccttgataaggtgaag 555
Db 488 tctcctaattgtgcgaagaattcagagacacattgtatcttcgtacaagaactgtag 547
QY 596 tagataacctctattgattctgttcgtccattatcaacaactctgtatgaac 655
Db 548 caatgatgtatgattggtttatccgttcgaacatttcggttaagcattgtgaagat 607
QY 656 tgccttgaagaatgcttgatattgttcgtccgaacaccttgacatgattactcttga 715
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QY 716 agtcattgctccagatgtatcatcaagcagattttgatgcagccctaagcctcgattaa 775
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QY 1016 ttctctgagagcggaagagcccttaaatctgttccctttaaaccgggggtgcagac 1075
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Db 1568 aagagcgtcaactgaagaagaagatgacatggaacttcaagaatattgttctaagcat 1627
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QY 1721 cgatcgagg 1729
Db 1688 ctaaggag 1696

RESULT 4
AAA97190
ID AAA97190 standard; cDNA; 1767 BP.
XX
AC AAA97190;
XX
DT 25-JAN-2001 (first entry)
XX
DE N. tabacum NIM1 homologue coding sequence SEQ ID NO: 1.
XX
KW Systemic acquired resistance; SAR; signal transduction cascade;
KW disease resistance; tobacco; tomato; canola; sunflower; sugarbeet;
XX potato; ss.
OS Nicotiana tabacum.
XX
FH Key Location/Qualifiers
FT CDS 1..1767
FT /tag= a
FT /product= "NIM1 homologue"
XX
PN MO200053762-A2.
XX
PD 14-SEP-2000.
XX
PF 07-MAR-2000; 2000OWC-EP01978.
XX
PR 09-MAR-1999; 99US-0265149.
XX
PA (NOVS ) NOVARTIS AG.
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI Salmeron JM, Weislo LJ, Willits MG, Mengiste T;
XX
DR WPI; 2000-594322/56.
XX
DR P-PsDB; AAB27301.
XX
PT Novel plant genes for enhancing systemic acquired resistance gene
PT expression and broad spectrum disease resistance in plants, are
PT homologues of Arabidopsis NIM1 gene -
XX
PS Claim 3; Page 68-70; 152pp; English.
XX
CC The present invention is concerned with the isolation of NIM1 homologues
CC and their coding sequences from Arabidopsis thaliana, Brassica napus,
CC Nicotiana tabacum, Lycopersicon esculentum, Beta vulgaris, Helianthus
CC annuus and Solanum tuberosum. NIM1 is one of the proteins involved in the
CC signal transduction cascade leading to systemic acquired resistance (SAR)
CC in plants. This gives the plants an increased resistance to disease. The
CC gene and protein can be used to produce transgenic plants resistant to
CC diseases caused by viruses, such as tobacco or cucumber mosaic virus,
CC ringspot virus, pelargonium leaf curl virus, red clover mottle virus,
CC tomato bushy stunt virus, fungi, including Phytophthora parasitica and
CC Peronospora tabacina, bacteria such as Pseudomonas syringae and P.
CC tabaci, insects, including aphids and lepidoptera and nematodes such as
CC Meloidogyne incognita. In particular they can be used against disease
CC organisms of maize.
XX

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XX 17-OCT-2000 (first entry)
DT Arabidopsis thaliana DNA fragment SEQ ID NO: 18587.
XX
DE
XX Hybridization assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301339.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
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RESULT 8
 ID AAV16851 standard; cDNA; 2104 BP.
 AC AAV16851;
 DT 17-AUG-1998 (first entry)
 DE Arabidopsis thaliana acquired resistance gene NPR1.
 KW NPR1 gene; acquired resistance; disease; plant pathogens; bacteria;
 KM mycoplasma; fungi; insects; nematodes; viruses; viroids;
 XX transgenic; ds.
 OS Arabidopsis thaliana.
 FH Key Location/Qualifiers
 FT CDS 93..1874
 FT /tag= a
 FT /product= acquired resistance protein
 FT /note= NPR1 gene
 PN MO9806748-A1.
 PD 19-FEB-1998.
 PE 08-AUG-1997; 97MO-US13994.
 PR 16-MAY-1997; 97US-0046769.
 PR 09-AUG-1996; 96US-0023851.
 PR 10-JUN-1997; 97US-0035166.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (UYDU-) UNIV DUKE.
 PI Ausubel FM, Cao H, Dong X, Glazebrook J;
 DR WPI, 1998-159458/14.
 DR P-PSDB; AAW46940.
 PT New isolated plant acquired resistance polypeptide gene - useful
 PT for, e.g. producing plants with increased resistance to pathogens

PT such as bacteria
 XX Claim 9; Fig 5; 127pp; English.
 PS The sequence is that of the acquired resistance gene NPR1. It may be
 CC used in the production of transgenic cells which can produce the encoded
 CC acquired resistance protein. Such transgenic plants cells are
 CC useful in the production of plants having an increased level
 CC of resistance against disease caused by plant pathogens, e.g.
 CC bacteria, mycoplasmas, fungi, insects, nematodes, viruses,
 CC and viroids.
 XX Sequence 2104 BP; 606 A; 431 C; 482 G; 585 T; 0 other;
 SQ

Query Match 20.7%; Score 422.2; DB 19; Length 2104;
 Best Local Similarity 56.0%; Pred. No. 9.3e-62;
 Matches 980; Conservative 0; Mismatches 703; Indels 66; Gaps 7;

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 QY 73 gccgacgagcgcgagctgagagcgctccgcgctctccgaacactcgcgcgag 132
 Db 201 gtactcaagcagctgtatgtatctcgtcgtcaattgtcttcaacagcttcgaatcgtc 260
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 QY 193 ggc 252
 Db 303 ctcccgacgc 362
 QY 253 ctgc 312
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 Db 1783 ggaagaag 1791

RESULT 10

AAV46275
ID AAV46275 standard; cDNA; 2011 BP.

AAV46275;

16-OCT-1998 (first entry)

A. thaliana NIM-1 cDNA variant #1.

NIM-1: noninducible immunity; systemic acquired resistance; SAR;
 pathogen: disease; protection: immunomodulated; plant; cereal; fruit;
 vegetable; virus; fungi; bacteria; insect; nematode; microbicide; ss.

Arabidopsis thaliana.
OS Synthetic.

Key Location/Qualifiers

CDS 43..1824

/tag= a
 /product= NIM-1
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 205..207

mutation

FT /tag= b

FT /note= "wild type TCC is replaced by GCC"

FT mutation

FT /tag= c

FT /note= "wild type TCG is replaced by GCG"

FT

PN WO9829537-A2.

XX 09-JUL-1998.

XX

XX 23-DEC-1997;

XX 97WO-EP07253.

XX 10-JAN-1997;

XX 97US-0035024.

XX 27-DEC-1996;

XX 96US-0034378.

XX (NOVS) NOVARTIS AG.

XX Friedrich IB, Molina Fernandez A, Ryals JA, Uknes SJ;

NIM1 preins act as dominant-negative regulators of the systemic acquired resistance (SAR) signal transduction pathway. The transgenic plants transformed with an altered NIM1 gene exhibits constitutive SAR expression which is higher in the transformed plants than in a wild-type plant. The products can be used for producing plants with a broad spectrum disease resistance. Overexpression of NIM1 mimics the effects of inducer compounds that induce constitutive immunity (CIM) phenotype in plants. The inventions can be used with plants such as rice, wheat, barley, rye, corn, potato, carrot, sweet potato, sugar beet, bean, pea, chichory, lettuce, cabbage, cauliflower, broccoli, turnip, radish, spinach, asparagus, onion, garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, quince, melon, plum, cherry, peach, nectarine, apricot, strawberry, grape, raspberry, blackberry, pineapple, avocado, papaya, mango, banana, soybean, tobacco, tomato, sorghum and sugarcane. The plants produced are resistant to plant pathogens such as viruses, viroids, fungi, bacteria, insects such as aphids and lepidoptera and nematodes. The plants produced can be used in agriculture.

SQ Sequence 1608 BP; 447 A; 340 C; 385 G; 436 T; 0 other;

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Best Local	Similarly	56.8%	Pred. No.	4.8e-60			
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RESULT 14			
AAV46276			
AAV46276 standard; cDNA; 1597 BP.			
AAV46276:			
16-OCT-1998 (first entry)			
A. thaliana N-terminal truncated NIM-1 variant cDNA #1.			
NIM-1: noninducible immunity; systemic acquired resistance; SAR;			
pathogen: disease; protection; immunomodulated; plant; cereal; fruit;			
vegetable; virus; fungi; bacteria; insect; nematode; microbicide; ss.			
Arabidopsis thaliana.			

RESULT 14
AAV46276
ID AAV46276 standard; cDNA; 1597 BP.
XX
XX
AC AAV46276;
XX
XX
DT 16-OCT-1998 (first entry)
XX
XX
A. thaliana N-terminal truncated NIM-1 variant cDNA #1.
DE
DE
XX
XX
KW NIM-1: noninducible immunity; systemic acquired resistance; SAR;
KW pathogen; disease; protection; immunomodulated; plant; cereal; fruit;
KW vegetable; virus; fungi; bacteria; insect; nematode; microbicide; ss.
XX
XX
OS Arabidopsis thaliana.

ID	AAV43662	standard	cdna: 1597 BP.
XX	AAV43662:		
DT	29-SEP-1998	(first entry)	
XX			
DE	Non-inducible immunity-1 (NIM1) protein variant 2 encoding CDNA.		
XX			
KW	transgenic plant; SAR; systemic acquired resistance; CIM; pathogen;		
KM	constitutive immunity; agriculture; variant; ss.		
XX			
OS	Arabidopsis thaliana.		
XX	Synthetic.		
EH			
FT	Key	Location/Qualifiers	
FT	CDS	1..1410	
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FT		/product- "NIM1 protein variant 2"	
FT		/note- "N-terminal deletion compared to wild-type NIM1 sequence"	
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XX	W09826082-A1.		
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PD	18-JUN-1998.		
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PE	12-DEC-1997;	97MO-EP07012.	
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PR	20-JUN-1997;	97US-00803177.	
PR	13-DEC-1996;	96US-0033177.	
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PR	27-DEC-1996;	96US-0034382.	
PR	10-JAN-1997;	97US-0034730.	
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PR	10-JAN-1997;	97US-0035022.	
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PA	(NOVS) NOVARTIS AG.		
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PI	Friedrich LB, Hunt MD, Lawton KA, Ryals JA, Steiner HY;		
PI	UKnes SJ;		
DR	WPI: 1998-348536/30.		
XX	P-PSDB; AAM61984.		
PT			
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PS	Claim 9; Pages 149-152; 205pp; English.		
XX			
CC	This CDNA encodes an altered form of the Arabidopsis thaliana non-		
CC	inducible immunity-1 (NIM1) protein. Sequences shown in AAV43661 to		
CC	AAV43665 represent variants of the NIM1 CDNA. The invention provides a		
CC	chimeric gene comprising a promoter active in plants operatively linked		
CC	to a DNA molecule that encodes an altered form of the NIM1 protein. Plant		
CC	cells stably transformed with a recombinant vector comprising such a		
CC	chimeric gene have a broad spectrum of disease resistance. The altered		
CC	NIM1 proteins act as dominant-negative regulators of the systemic		
CC	acquired resistance (SAR) signal transduction pathway. The transgenic		
CC	plants transformed with an altered NIM1 gene exhibits constitutive SAR		
CC	expression which is higher in the transformed plants than in a wild-type		
CC	plant. The products can be used for producing plants with a broad		
CC	spectrum disease resistance. Overexpression of NIM1 mimics the effects		
CC	of inducer compounds that induce constitutive immunity (CIM) phenotype		
CC	in plants. The inventions can be used with plants such as rice, wheat,		
CC	barley, rye, corn, potato, carrot, sweet potato, sugar beet, bean, pea,		
CC	chicory, lettuce, cabbage, cauliflower, broccoli, turnip, radish,		
CC	squash, asparagus, onion, garlic, eggplant, pepper, celery, carrot,		
CC	cherry, peach, nectarine, apricot, strawberry, grape, raspberry,		
CC	blackberry, pineapple, avocado, papaya, mango, banana, soybean, tobacco,		
CC	tomato, sorghum and sugarcane. The plants produced are resistant to		

CC plant pathogens such as viruses, viroids, fungi, bacteria, insects such
CC as aphids and lepidoptera and nematodes. The plants produced can be used
CC in agriculture.

SQ Sequence 1597 BP; 467 A; 304 C; 381 G; 445 T; 0 other;

Query Match	20.1%;	Score 409.2;	DB 19;	Length 1597;
Best Local Similarity	58.3%;	Pred. No. 1.3e-59;		
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 Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 2104)
 AUTHORS Cao, H., Glazebrook, J., Clarke, J. D., Volk, S. and Dong, X.
 TITLE The Arabidopsis NPR1 gene that controls systemic acquired
 resistance encodes a novel protein containing ankyrin repeats
 JOURNAL Cell 88 (1), 57-63 (1997)
 MEDLINE 97148688
 REFERENCE 2 (bases 1 to 2104)
 AUTHORS Cao, H., Glazebrook, J., Clarke, J. D., Volk, S. and Dong, X.
 TITLE Direct Submission

JOURNAL Submitted (30-OCT-1996) DCMB Group, Botany, Duke University, LSRC
Building, Research Dr., Durham, NC 27708-1000, USA

FEATURES

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 LOCUS AR087502 2011 bp DNA PAT 07-SEP-2000
 DEFINITION Sequence 6 from patent US 5986082.
 ACCESSION AR087502
 VERSION AR087502.1 GI:10014265
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 2011)
 AUTHORS Dknes,S,Joseph, Hunt,M,Denise, Steiner,H, and Ryals,J,Andrew.
 TITLE Altered forms of the NIM1 gene conferring disease resistance in plants
 JOURNAL Patent: US 5986082-A 6 16-NOV-1999;
 FEATURES Location/Qualifiers
 source 1..2011
 BASE COUNT 563 a 417 c 472 g 559 t
 ORIGIN
 Query Match 20.6%; Score 420.6; DB 9; Length 2011;
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SQ Sequence 1767 BP; 512 A; 328 C; 434 G; 493 T; 0 other;

Query Match **27.6%**; **Score.563.4**; **DB 21**; **Length 1767**;

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Db	641		
		tgccttcaagctgaattgagattatgttcaagttctaatgttgatactcaacccttgata	700
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RESULT

RESOL 3
AAV16852
ID AAV16852 standard; cDNA: 2172 BP

AC AAV16852;

DT 17-AUG-1998 (first entry)

DE *Nicotiana glutinosa* NPR1 homologue.

NPRI gene; acquired resistance; disease; plant pathogens; bacteria;
KW
mycoplasma; fungi; insects; nematodes; viruses; viroids;
KW
transgenic; homologue; ds.

OS Nicotiana glutinosa.

xx	Key	Location/Qualifiers
FH		

FT CDS

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FT
/*tag= a

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FT₂ /product= acquired resistance polypeptide

FT /note= NPRI homologue

XX

PN WO9806748-A1.

XX
10-SEP-1000

PD 19-FEB-1998.
vvy

XX
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PF
11/55T-50Y-80
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XX

AA 16-MAY-1997; 97US-0046769.

PR	09-AUG-1996;	96US-0023851.
PR	09-AUG-1996;	96US-0023851.

PR 10-JAN-1997; 97US-0035166.

XX

PA (GEHO) GEN HOSPITAL CORP.

PA (UYDJ-) UNIV DUKE.

XX
DT Augsburg EM Cao H Dong Y Clatsbrook T.

PI Ausubel FM, Cao H, Dong X, Glazebrook J, XX

XX
DR WPI: 1998-159458/14.

DR P-PSDB; AAW46942.

XX
1955, November 12

PT New isolated plant acquired resistance poly

PT for, e.g. producing plants with increased

PT such as bacteria

XX
XX
XX

Class 10. Etc 7. 1928. English

PS
XX
claim 10; Fig 7; 12/pp; English.

W


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RESULT 3
US-08-996-685-6
: Sequence 6, Application US/08996685
: Patent No. 6031153
GENERAL INFORMATION:
APPLICANT: Ryals, John
APPLICANT: Friedrich, Leslie
APPLICANT: Uknes, Scott
APPLICANT: Molina, Antonio
APPLICANT: Ruess, Wilhelm
APPLICANT: Knauf-Belter, Gertrude
APPLICANT: Kung, Ruth
APPLICANT: Kessmann, Helmut
APPLICANT: Oostendorp, Michael
TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:

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ADDRESSSEE: No. 6031153artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6031153ch Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,685
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/761,543
FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,378
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,024
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/875,015
FILING DATE: 16-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21215/PL/CGC1912125
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2011 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORGANISM: Arabidopsis thaliana
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LOCATION: 1..2011
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US-08-996-685-6

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent'n Release #1.0, Version #1.30
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APPLICATION NUMBER: US/08/996,685
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/761,543
FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,378
FILING DATE: 27-DEC-1996
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/875,015
FILING DATE: 16-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 7:
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LENGTH: 2011 base pairs
TYPE: nucleic acid
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TOPOLOGY: linear
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LOCATION: 43..1824
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OTHER INFORMATION: residues."
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OTHER INFORMATION: changed from T's to G's compared to wild-type sequence."

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 Db 1243 GAAGCAAAACGAGAAATTCCTAGAGATGTTCTCCCTCTTTTGCATGCGCGCAT 1302
 Oy 1273 agctacagagagaggttctgtatcttgaacacagttgtcttgcgaagatagttt 1332
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 Oy 1333 ccgagtgagagagagtgatgcatatcttcaagtgtgatacttgaatttaac 1392
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 Oy 1510 gtgagagctcgagaaagcttttcccgagtgctgcaagtgctgcgaagaatcatg--- 1566
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 Db 1603 TGTGAGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1662
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 Oy 1735 cgaccaag 1743
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RESULT 5

US-08-989-478-11
 : Sequence 11, Application US/08989478
 : Patent No. 5986082

GENERAL INFORMATION:

APPLICANT: Uknes, Scott
 APPLICANT: Hunt, Michelle
 APPLICANT: Steiner, Henry-York
 APPLICANT: Ryals, John
 TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESS: No. 5986082art's Corporation
 STREET: 3054 Cornwalls Road
 CITY: Research Triangle Park
 STATE: No. 5986082th Carolina
 COUNTRY: USA
 ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/989,478
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/033,177
 FILING DATE: 13-DEC-1996

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/034,379
 FILING DATE: 27-DEC-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/034,382
 FILING DATE: 27-DEC-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/034,730
 FILING DATE: 10-JAN-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/035,021
 FILING DATE: 10-JAN-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/035,022
 FILING DATE: 10-JAN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Meigs, J. Timothy
 REGISTRATION NUMBER: 38,241
 REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919) 541-8587
 TELEFAX: (919) 541-8689
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1608 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 43..1608
 OTHER INFORMATION: /product="Altered form of NIM1"
 OTHER INFORMATION: /note="C-terminal deletion compared to wild-type NIM1."
 US-08-989-478-11

Query Match 20.2%; Score 411.8; DB 2; Length 1608;
 Best Local Similarity 56.8%; Pred. No. 1.7e-80;
 Matches 886; Conservative 0; Mismatches 622; Indels 51; Gaps 5;

Oy 13 accagcagctacccaacgcttctcgcagctgagacagcgctccgtgagagagagagc 72
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 Db 151 GTCACACCGGACGACGATGATGCTGCTGCAATGCTCTCCACAGCTTCAAGTCCGTC 210
 Oy 133 ttcgc 192
 Db 211 TTGACTCCCGGAGATGATTC-----TACAGGACGCTTAAGCTTCT 252
 Oy 193 ggc 252
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RESULT 6
US-08-996-685-11
Sequence 11, Application US/08996685
Patent No. 6031153
GENERAL INFORMATION:
APPLICANT: Ryals, John
APPLICANT: Friedrich, Leslie
APPLICANT: Uknes, Scott
APPLICANT: Molina, Antonio
APPLICANT: Ruesch, Wilhelm
APPLICANT: Knauf-Belter, Gertrude
APPLICANT: Kung, Ruth
APPLICANT: Kessmann, Helmut
APPLICANT: Oostendorp, Michael
TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6031153artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6031153th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/996, 685
APPLICATION NUMBER: US/08/996, 685
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/761,543
FILING DATE: 6-DEC-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/034,378
FILING DATE: 27-DEC-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/035,024
FILING DATE: 10-JAN-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/875,015
FILING DATE: 16-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21215/P1/GC1912
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8587
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1608 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Melgs, J. Timothy
REGISTRATION NUMBER: 38, 241
REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1597 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1410
OTHER INFORMATION: /product= "Altered form of NIMI"
OTHER INFORMATION: /note= "N-terminal deletion compared to wild-type NIMI
sequence."
US-08-989-478-9

Query Match	20.1%	Score 409.2	DB 2	Length 1597
Best Local Similarity	58.3%	Pred. No. 6.1e-80		
Matches	808	Conservative	0	Mismatches 548; Indels 30; Gaps 4;
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QY	436	gcgcgctgcctctgctgcgcagagacacgagcccaagctcgggtgcaccccgctgcg	495	
Db	64	GAAGTTTCTGAATGGACGACAGCAGAAATTCCTCCACGTGGCTGGCGCGCGGTGGAT	123	
QY	496	ttcaatcgcgacgagctcctcttcgcgcctccacacctccagctgcgcgagctcacaacctc	555	
Db	124	TTTCATGTTGGAGGTTCTCTCATTTTGGCTTTCACTTTCATCTTCAAGATCCCGTAATTAATTA	183	
QY	556	ttccagcgcgctctcctctgtagtgccttgataaggttgaaagtatagataacctctatgtac	615	
Db	184	TATCAAGAGGCATTTTGTGACGTTGTAGCAAAAGTGTGTAATGAGAGACCATTTGGTTATA	243	
QY	616	ttatctgtctccaaattatgcaacaacatcttcataaactctctgaaagatgacctggt	675	
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QY	676	atggtagctcggtcaaaccttgacatgatacttactcttgagaagctcatcttgctccacatgt	735	
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QY	916	ggcgtcgaacatigtgactccaataatcaacagcagcttttgatctcgcacttgcaat	975
Db	532	GCTGTGCATATTGTCATGTGAAGACCGGACAGAGATCTTTAAACTTGATTTGCCAT	591
QY	976	gtatacatgaaacccaagaggtatactgtcttcacatgtctgcgagcgcaagag	1035
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QY	1096	ggsgaagaagcgyttcaatctcmetaaagaactaacaacaaaggagatbaacttgggt	1155
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QY	1156	accgaagaagaaacaccttccaanaagatagttatgatatgaatcttgaagaact	1215
Db	772	CCGAGCAATGCAAGCATTTCTCTCAAGGCCGCACTGTGTGAAATATCTACAGCAATA	831
QY	1216	gaagaagaaggaccacaaccccgagagaagcaatcagttcttccttgcaatgcaagt	1275
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QY	1276	ctacagaggaaggttgcctgtctcttgaaaccgagttgctttggcaagataatgttccg	1335
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QY	1396	---ggtctgtgtgcaatccactcctgaaagcaacgagacaactgttgatctaaatga	1455
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Db	1132	GAACTCGGGAACAGATTCCTCCCGCGGTGTTCGGCAGTGCTCGACCAAGATATGAACGT	1191
QY	1567	gatatgataaactgtatccggtttccctcgcgaagagacagttccgcg-----gagaag	1617
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QY	1618	aggaagaaggtttcaatgacccgcgagagatggtcttcagaagaagcattccacaggaagaag	1677
Db	1252	AAGCAAAAGTACATGGAATACAAAGAGACCTTAAGAAAGGCCCTTTAAGTAGAGGACAAATTG	1311
QY	1678	gagaatpacaggttcgagggcctctgtctgtctgcatacgcatacgatcggggccattcga	1737
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QY	1738	ccaagg 1743	
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RESULT 8
US-08-996-685-9
; Sequence 9, Application US/08996685
; Patent No. 6031153
; GENERAL INFORMATION:

Db 592 GTCAACCATAGAAATCCAGGGGATATACGGTCTCATGTTCTCGATCGGAGAG 651
 QY 1036 cctaataatcgtctccctttaaaccagggtcgcacagatgatactgacat 1095
 Db 652 CCACAATGATATCTATCTCTATGAAAAAGTGCAGATGCATGCAAGCAACTTTGAA 711
 QY 1096 ggggaaagaggttcaatctcaaaagactaaacaaagggtacttgggtt 1155
 Db 712 GGTGAACCCGACTCANGATGCAAAACAGCCACTATGCGGTTGATTAATATTC 771
 QY 1156 accgaagaagaaacccctccaaagaatgattatgataatactgagcaagct 1215
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 Db 832 GACAAACGAGAACAAATTCCTAGAGATGTCTCCCTCTTTGGCGTGGCCGATGAA 891
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RESULT 10 US-08-996-685-13

Sequence 13, Application US/0896685

Patent No. 6031153

GENERAL INFORMATION:

APPLICANT: Ryals, John

APPLICANT: Friedrich, Leslie

APPLICANT: Uknes, Scott

APPLICANT: Molina, Antonio

APPLICANT: Rues, Wilhelm

APPLICANT: Knaut-Belter, Gertrude

APPLICANT: Kuesmann, Helmut

APPLICANT: Oostendorp, Michael

TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6031153artis Corporation

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: No. 6031153th Carolina

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/996.685

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/761,543

FILING DATE: 6-DEC-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/034,378
 FILING DATE: 27-DEC-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/034,379
 FILING DATE: 27-DEC-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/034,382
 FILING DATE: 27-DEC-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/034,730
 FILING DATE: 10-JAN-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/035,021
 FILING DATE: 10-JAN-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/035,022
 FILING DATE: 10-JAN-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/035,024
 FILING DATE: 10-JAN-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/875,015
 FILING DATE: 16-JUL-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PE/5-21215/P1/GC1912
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919) 541-8587
 TELEFAX: (919) 541-8689
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1194 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1194
 OTHER INFORMATION:
 OTHER INFORMATION: /note="N-terminal/C-terminal chimera."
 US-08-996-685-13

Query Match 19.6%; Score 400.4; DB 3; Length 1194;
 Best Local Similarity 59.8%; Pred. No. 4.4e-78;
 Matches 715; Conservative 0; Mismatches 466; Indels 15; Gaps 2;

QY 376 gagcgctgagcgctgctgctgactacactcaagcgcgctgagcgactgcccgaag 435
 Db 4 GATTCGCTGTGACCTGTTTGGCTTTATGTTACAGCAGCAGATGAGACCGGCTTAA 63
 QY 436 gcgagctgctctgctgctgagagagactgcccacgttggtggtccaccgcccgcg 495
 Db 64 GAGATTCTGAATGCGCAACAGAGATGCTGCGACGCTGCGCGCGGGGGTGAAT 123
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RESULT 11
US-08-989-478-15
Sequence 15, Application US/08989478
Patent No. 5986082
GENERAL INFORMATION:
APPLICANT: Unnes, Scott
APPLICANT: Hunt, Michelle
APPLICANT: Steiner, Henry-John
APPLICANT: Ryals, John
TITLE OF INVENTION: ALTERED FORMS OF THE NIMI GENE CONFERRING
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5986082artis Corporation

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STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 5986082th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,478
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..786
OTHER INFORMATION: /product= "Altered form of NIMI."
OTHER INFORMATION: /note= "Ankyrin domains of NIMI."
US-08-989-478-15
Query Match 13.0%; Score 264.8; DB 2; Length 786;
Best Local Similarity 60.8%; Pred. No. 9e-49;
Matches 456; Conservative 0; Mismatches 282; Indels 12; Gaps 1;

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DB 757 AGTCATCAG 786

RESULT 13
US-08-989-478-1

Sequence 1, Application US/08989478
Patent No. 5986082

GENERAL INFORMATION:

APPLICANT: Uknes, Scott
APPLICANT: Hunt, Michelle
APPLICANT: Steiner, Henry-York
APPLICANT: Ryals, John
TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
NUMBER OF SEQUENCES: 32
DISEASE RESISTANCE IN PLANTS
CORRESPONDENCE ADDRESS:
ADDRESS: No. 5986082artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 5986082th Carolina
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,478

FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5655 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: exon
LOCATION: 2787..3347
OTHER INFORMATION: /product= "1st exon of NIM1"
FEATURE:
NAME/KEY: exon
LOCATION: 3427..4162
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LOCATION: join(2787..3347, 3427..4162, 4271..4474, 4586..4866)
US-08-989-478-1

Query Match 12.7%; Score 258.4; DB 2; Length 5655;
Best Local Similarity 60.0%; Pred. No. 4.6e-47;
Matches 455; Conservative 0; Mismatches 291; Indels 12; Gaps 1;

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QY 914 acgcgctgaacattgtagctccaaatatacaacagagctttagatctgcagattgag 973
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DB 4127 AATGAGATGACGCTGCTGATCTTGAATAAGAGGT 4164

RESULT 14
US-08-996-685-1
Sequence 1, Application US/08996685
Patent No. 6031153

GENERAL INFORMATION:
APPLICANT: Ryals, John
APPLICANT: Friedrich, Leslie
APPLICANT: Uknes, Scott
APPLICANT: Molina, Antonio
APPLICANT: Ruess, Wilhelm
APPLICANT: Knauf-Belter, Gertrude
APPLICANT: Kung, Ruth
APPLICANT: Kessmann, Helmut
APPLICANT: Oostendorp, Michael
TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6031153artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6031153th Carolina
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,685
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/761,543
FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,378
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,024
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/875,015
FILING DATE: 16-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5655 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: exon
LOCATION: 2787..3347
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FEATURE:
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NAME/KEY: CDS
LOCATION: join(2787..3347, 3427..4162, 4271..4474, 4586..4866)
US-08-996-685-1

Query Match 12.7%; Score 258.4; DB 3; Length 5655;
Best Local Similarity 60.0%; Pred. No. 4.6e-47;
Matches 455; Conservative 0; Mismatches 291; Indels 12; Gaps 1;

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QY 614 tcttactgttgcacacttaagcaacaatctgcagaaactgtctgaagaatgtcctg 673
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RESULT 15
 US-08-880-179-2
 Sequence 2, Application US/08880179
 Patent No. 6091004
 GENERAL INFORMATION:
 APPLICANT: Ryals, John
 APPLICANT: Delaney, Terry
 APPLICANT: Friedrich, Leslie
 APPLICANT: Weymann, Kristianne
 APPLICANT: Layton, Kay
 APPLICANT: Ellis, Daniel
 APPLICANT: Uknes, Scott
 APPLICANT: Jesse, Taco
 APPLICANT: Vos, Pieter
 TITLE OF INVENTION: GENE ENCODING A PROTEIN INVOLVED IN THE
 TITLE OF INVENTION: SIGNAL TRANSDUCTION CASCADE LEADING TO SYSTEMIC ACQUIRED RESIS
 TITLE OF INVENTION: IN PLANTS
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 6091004artis Corporation
 STREET: 520 White Plains Road, P.O. Box 2005
 CITY: Tarrytown
 STATE: New York
 COUNTRY: USA
 ZIP: 10591
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/880,179
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Meigs, J. Timothy
 REGISTRATION NUMBER: 38,241
 REFERENCE/DOCKET NUMBER: CGC 1909
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919) 541-8587

TELEFAX: (919) 541-8689
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5655 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHEetical: NO
 ANTI-SENSE: NO
 FEATURE:
 NAME/KEY: exon
 LOCATION: 2787..3347
 OTHER INFORMATION: /product= "1st exon of NIM1"
 FEATURE:
 NAME/KEY: exon
 LOCATION: 3427..4162
 OTHER INFORMATION: /product= "2nd exon of NIM1"
 FEATURE:
 NAME/KEY: exon
 LOCATION: 4271..4474
 OTHER INFORMATION: /product= "3rd exon of NIM1"
 FEATURE:
 NAME/KEY: exon
 LOCATION: 4586..4866
 OTHER INFORMATION: /product= "4th exon of NIM1"
 FEATURE:
 NAME/KEY: CDS
 LOCATION: join(2787..3347, 3427..4162, 4271..4474, 4586..4866)
 US-08-880-179-2

Query Match 12.7%; Score 258.4; DB 3; Length 5655;
 Best Local Similarity 60.0%; Pred. No. 4.6e-47;
 Matches 455; Conservative 0; Mismatches 291; Indels 12; Gaps 1;
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 Job time: 6285 sec

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